

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2005, 13:45:21 ; Search time 8024 Seconds

(without alignments)  
11540.127 Million cell updates/sec

Title: US-10-602-898A-1

Perfect score: 1629  
Sequence: 1 cctgacgtacgcgtgttg.....cagaagataaaacgctacta 1629

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_ste.\*
- 11: gb\_sv.\*
- 12: gb\_un.\*
- 13: gb\_vl.\*
- 14: gb\_hgt.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1629	100.0	1629	15	ATU12232
2	1536.4	94.3	1619	15	AY045860 Arabidopsis
3	1132.4	69.5	1134	6	Q0804428 Sequence
4	1113.8	68.4	1128	15	BT020366 Arabidopsis
5	811.8	49.8	125502	15	AT04120 Arabidopsis
6	811.8	49.8	195921	15	ATCHRIV91 Arabidopsis
7	661.6	40.6	1526	15	AF170921 Pisum sat
8	656.4	40.3	1430	15	NT284820 N.tabacum m
9	654.8	40.2	1600	15	AF249743 Arabidopsis
10	651	40.0	1434	15	NT284821 N.tabacum m
11	644.8	39.6	1505	15	NPY09513 Arabidopsis
12	642.4	39.4	1540	15	AF14114 Solanum t
13	641.2	39.4	1560	15	NTGFRTEET Arabidopsis
14	640.8	39.3	1524	15	STGB1GENE Arabidopsis
15	640.6	39.3	1611	15	AF145976 Pisum sat
16	576.4	35.4	1664	15	OSGPROTBS Arabidopsis
17	558.8	34.3	1671	15	ZMU12233 Zea mays GT
18	558.2	34.3	1688	15	AB090160 Triticum

19	551.8	33.9	1470	15	AF033357 Avena fat
20	422	25.9	1157	15	BT017412 Zea mays
21	385.8	23.7	722	15	NTU22524 Arabidopsis
22	344.8	21.2	1777	15	PPA428878 Arabidopsis
23	284.4	17.5	4090	15	AF533440 Pisum sat
24	257.4	15.8	110000	15	AP008209 261
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26	257.4	15.8	139187	15	AC133930 Oryza sat
27	229	14.1	98126	14	AP008019 Arabidopsis
28	187	11.5	1536	15	PPA512651 Arabidopsis
29	167.8	10.3	1106	15	AY599846 Arabidopsis
30	167.6	10.3	1431	15	AF306565 Arabidopsis
31	151.2	9.3	3259	5	BC076910 Arabidopsis
32	151	9.3	2260	15	AB072452 Arabidopsis
33	147.8	9.1	3947	15	AY219172 Arabidopsis
34	146.4	9.0	1982	2	AK114926 Arabidopsis
35	146	9.0	1394	2	LFBGTPB Arabidopsis
36	145.6	8.9	1044	2	DGGBS Arabidopsis
37	144.8	8.9	3112	5	BC084263 Arabidopsis
38	144.6	8.9	2634	15	CPU95139 Arabidopsis
39	144.4	8.9	1026	2	AY389499 Arabidopsis
40	144.4	8.9	1619	5	AF277161 Arabidopsis
41	143.8	8.8	3354	15	AB188197 Arabidopsis
42	143.2	8.8	1655	5	XLKGBETA1 Arabidopsis
43	142.4	8.7	1611	5	CR761620 Arabidopsis
44	142.2	8.7	1600	15	AY661671 Arabidopsis
45	140.6	8.6	1730	2	LSGPBS Arabidopsis

## ALIGNMENTS

RESULT 1	ATU12232	1629 bp	mRNA	linear	PLN 12-OCT-1994
LOCUS	Arabidopsis thaliana Columbia GTP binding protein beta subunit				
DEFINITION	(AGB1) mRNA, complete cds.				
ACCESSION	U12232				
VERSION	U12232.1				
KEYWORDS	GI:557693				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	1 (bases 1 to 1629)				
AUTHORS	Weiss, C.A., Garnaat, C.W., Mukai, K., Hu, Y. and Ma, H.				
TITLE	Isolation of cDNAs encoding guanine nucleotide-binding protein beta-subunit homologues from maize (ZGB1) and Arabidopsis (AGB1)				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 91 (20), 9554-9558 (1994)				
PUBMED	7937804				
REFERENCE	2 (bases 1 to 1629)				
AUTHORS	Ma, H.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-JUL-1994) Hong Ma, Delbruck, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724-2212, USA				
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ORIGIN

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Db 1 CCTGACGTAGCAGCGTGTGTGCTTGTGACTGATCTTCTCTCAAGCTTTTTTAATCTCTC 60  
Qy 61 TCTCTTTTCCACAGTAATTCGCCCAAAATCCATCTCTTAGGGTTCGATCCCTCTCTC 120  
Db 61 TCTCTTTTCCACAGTAATTCGCCCAAAATCCATCTCTTAGGGTTCGATCCCTCTCTC 120  
Qy 121 AATCATGAACCTTCTCTCTAGACCCCAAGTTTCCCTTTTATTTGATCGGCG 180  
Db 121 AATCATGAACCTTCTCTCTAGACCCCAAGTTTCCCTTTTATTTGATCGGCG 180  
Qy 181 ACGGAGAACCTTAAGTCTCGGAATGTCGTCTCCGAGCTCAAGAAACGCCACGCC 240  
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Db 241 GTCGTACGGAGACCGTTAAATACCTCCGTGACACAGCTTAGACAGACGCTCCAGCTC 300  
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Db 301 CTCGATACCGATGTGGCGAGGTATTACGGCGGCAAGACGCTACTCGGGTGAGCTTCGGA 360  
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Db 361 GCAACGGATCTGTTGTTGTCGTACTCTTCAGGGACACACCGGAAAGGTTTATTCATTA 420  
Qy 421 GATTGGACACCGGAGAGAACCGGATTCAGTGTCATCTCAAGATGGGAGATTAATCGTG 480  
Db 421 GATTGGACACCGGAGAGAACCGGATTCAGTGTCATCTCAAGATGGGAGATTAATCGTG 480  
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Qy 601 TCTATCTTTAGCCTTAGCTCAACCGCGGACAAAGGATGAACTGTACCGGTTTCAAGATG 660  
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Qy 661 CTCACGTGTACAGGGATATGTTTCGTGCTGTCAGTATGTCCTCAAAATGAGGATGCCAC 720  
Db 661 CTCACGTGTACAGGGATATGTTTCGTGCTGTCAGTATGTCCTCAAAATGAGGATGCCAC 720  
Qy 721 CTTATCACCAAGTTACAGGTGATCAAACTTGATCTTATGGGATGTAACTACTGGTCTCAAA 780  
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Db 781 ACTTCTGTTTTTGGCGGTGAATTTCACTCTGGACATACCTGCTGATGACTAAAGCGTCTCA 840  
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Db 841 ATCAGTGGATCAAAACCCAACTGGTTTATATCTGGTTTCATGCGATTCACAGACCGTTG 900  
Qy 901 TGGGACACTCGTCTGTCGAAGCCGAGCAGTGGTACCTTTTCATGTCACGAGGAGATGTT 960  
Db 901 TGGGACACTCGTCTGTCGAAGCCGAGCAGTGGTACCTTTTCATGTCACGAGGAGATGTT 960  
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Db 1021 TGCAGGCTGTATGACATAAAGGACTGGTCACCACTCCAGGCTCTATCAGCCACATGGTAT 1080  
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Db 1081 GGTGAGAACCGACCTGTCACTCCATTTGCATTTCTCTGTGTCAGGAGACTTTCTTTTCGCT 1140  
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Qy 1201 GATTGCGGATTTACAGCAGGATTCACACAGGAATAGATTAAGCTGTTTGGGTTGTCAGCA 1260  
Db 1201 GATTGCGGATTTACAGCAGGATTCACACAGGAATAGATTAAGCTGTTTGGGTTGTCAGCA 1260  
Qy 1261 GATGGAAGTGCATTTGCTACAGGAAGTTGGGATTTCAAATCTAAAGATATGGCGCTTTGGA 1320  
Db 1261 GATGGAAGTGCATTTGCTACAGGAAGTTGGGATTTCAAATCTAAAGATATGGCGCTTTGGA 1320  
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Db 1441 AAATAGTGGAGTGGTTAGAAGAAATTAACCTTCCCTTTTGTAGTGTGCTTTGATTATTT 1500  
Qy 1501 ATTTCTTCATTTGGGAATCAACTCTTCAACACGCTACTCAATGTGAATTTCTGTAATCAA 1560  
Db 1501 ATTTCTTCATTTGGGAATCAACTCTTCAACACGCTACTCAATGTGAATTTCTGTAATCAA 1560  
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Db 1561 TTGTGTACCCACCACTGCTTTTACTTACTATCTCTTCAATATTTGAACGAGAGATAAA 1620  
Qy 1621 ACGCTACTA 1629  
Db 1621 ACGCTACTA 1629

RESULT 2  
AY045860  
LOCUS  
DEFINITION Arabidopsis thaliana At4g34460 mRNA sequence.  
ACCESSION AY045860  
VERSION AY045860.1 GI:15028006  
KEYWORDS FLU CDNA.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi8.



QY	1033	GACATAAGGACTGTGTCACCAACTCCAGGTCTATACAGCCACATGCTGATGCTGAGAACCGGA	1092
Db	1065	GACATAAGGACTGTGTCACCAACTCCAGGTCTATACAGCCACATGCTGATGCTGAGAACCGGA	1124
QY	1093	CCTGTACCTCCATTCGATCTCTCTGTGTCAGGAGACCTCTTTTCGCTGGCTATGCGGAGC	1152
Db	1125	CCTGTACCTCCATTCGATCTCTCTGTGTCAGGAGACCTCTTTTCGCTGGCTATGCGGAGC	1184
QY	1153	AACAACTTGTCTAGCTTTGGGATACCTCTTTGGGAGAGGTTGTATTTGGATTTGGGATTA	1212
Db	1185	AACAACTTGTCTAGCTTTGGGATACCTCTTTGGGAGAGGTTGTATTTGGATTTGGGATTA	1244
QY	1213	CAGCAGGATTCACACAGGAATAGAAATAGCTGTGTTGGGGTTGTACAGCAGATGGAAGTGA	1272
Db	1245	CAGCAGGATTCACACAGGAATAGAAATAGCTGTGTTGGGGTTGTACAGCAGATGGAAGTGCC	1304
QY	1273	TTGTGTACAGGAAGTTGGGATTCAAATCTAAAGATATGGCGTTTGGAGGACACAGGAGA	1332
Db	1305	TTGTGTACAGGAAGTTGGGATTCAAATCTAAAGATATGGCGTTTGGAGGAC - CAGGAGA	1363
QY	1333	GTGATTTTGAAGAAGATTAAACGAAAGTAGGAGTCACTCTCCAGTTCTTGGTTAAATATA	1392
Db	1364	GTGATTTTGAAGAAGATTAAACG - AAAGTAGGAGTCACTCTCCAGTTCTTGGTTAAATATA	1422
QY	1393	TTCTGTAGTCGGGAAGTAGGTTTCGGTTTGTGGAAAGGTTGTTGGTTGAAATAGTGGAGT	1452
Db	1423	TTCTGTAGTCGGGAAGTAGGTTTCGGTTTGTGGAAAGGTTGTTGGTTGAAATAGTGGAGT	1482
QY	1453	GTTTGAAGAATTAACCTTCCCTTTTGTAGTGCTTTTGTGATTTATTTATTTCTTCATTG	1512
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Db	1603	CA 1604	
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DEFINITION	Sequence 839 from Patent WO2004035798.		
ACCESSION	CQ804428		
VERSION	CQ804428.1	GI:47110848	
KEYWORDS	Arabidopsis thaliana (thale cress)		
SOURCE	Arabidopsis thaliana		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Inze, D., de Veylder, L. and Vlieghe, K.		
AUTHORS	Identification of novel e2f target Genes and use thereof		
TITLE	Patent: WO 2004035798-A 839 29-APR-2004;		
JOURNAL	CropDesign N.V. (BE)		
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Best Local Similarity	99.9%	Pred. No. 2.8e-313;	
Matches 1133;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
QY	208	ATGTCGTCTCCGAGCTCAAGAAGCCACGCCGCTCGCTACGAGACCGCTTAATAACCTC	267
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QY	268	CGTGAACGAGCTTACAGAGACGCTCCAGTCTCTCGATACCGATGTGGCCAGGTATTCA	327
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QY	328	CGCGCGAAGGACCTACTCGGGTGAGCTTCGGAGCAACGGATCTGTTGTTGTCGTA	387
Db	121	CGCGCGAAGGACCTACTCGGGTGAGCTTCGGAGCAACGGATCTGTTGTTGTCGTA	180
QY	388	CTTCAGGGACACACCGGAAAGTTTATTCATTAGATTGGACACCGGAGAGGAAACCGGATT	447
Db	181	CTTCAGGGACACACCGGAAAGTTTATTCATTAGATTGGACACCGGAGAGGAAACCGGATT	240
QY	448	GTCAAGTGCATCTCAAGATGGGAGATTAAATCGTGTGGAAATGCTCTAAACGAGTCAGAAACT	507
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Db	301	CATGCTATTAACCTCCCTTGTGATGGTTATGACATGTGCTTCTCTCCAAATGGTCAG	360
QY	568	TCGGTTGCGTGTGGATTAGACAGATGTATGTTCTATCTTTAGCCTTAGCTCAACCGCG	627
Db	361	TCGGTTGCGTGTGGATTAGACAGATGTATGTTCTATCTTTAGCCTTAGCTCAACCGCG	420
QY	628	GACAAAGATGGAACTGTACCGGTTTCAAGAAATGCTCACTGGTCAACGAGGATATGTTTCG	687
Db	421	GACAAAGATGGAACTGTACCGGTTTCAAGAAATGCTCACTGGTCAACGAGGATATGTTTCG	480
QY	688	TGCTGTCAAGTATGCCAAATGAGGATGCCACCTTATCACCAGTTCAGGTGATCAAACT	747
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QY	748	TGTATCTTATGGGATGTAACTACTGCTCTCAAACTTCTGTTTGGCGGTGAATTTTCAG	807
Db	541	TGTATCTTATGGGATGTAACTACTGCTCTCAAACTTCTGTTTGGCGGTGAATTTTCAG	600
QY	808	TCTGGAATACTGCTGATGTACTAAGCGTCTCAATCAGTGGATCAAAACCCAACTGGTTT	867
Db	601	TCTGGAATACTGCTGATGTACTAAGCGTCTCAATCAGTGGATCAAAACCCAACTGGTTT	660
QY	868	ATATCTGTTTCATCGGATTCACAGACGCTGTGGGACACTCGTGTGCAAGCCGACGA	927
Db	661	ATATCTGTTTCATCGGATTCACAGACGCTGTGGGACACTCGTGTGCAAGCCGACGA	720
QY	928	GTGCGTACTCTTTCATGCTCAGAGGAGATGTTAATACGGTCAAGTCTCTTTCCGATGGG	987
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QY	988	TATAGATTGGGACTGGATCAGACGATGGAAACATGCGGCTGTATGATAGATAGGACTGGT	1047
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QY	1048	CACCACTCCAGGCTATCAGCCACATGCTGATGCTGAGAACGCGCTGTCCCTCCATT	1107
Db	841	CACCACTCCAGGCTATCAGCCACATGCTGATGCTGAGAACGCGCTGTCCCTCCATT	900
QY	1108	GCATTTCTGCTCAGGAGACTCTTTTTCGCTGGCTATGCGAGCAACAACTTTGCTAC	1167
Db	901	GCATTTCTGCTCAGGAGACTCTTTTTCGCTGGCTATGCGAGCAACAACTTTGCTAC	960
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Db	1021	AGGAATAGAAATAGCTGTTTGGGGTGTGTCAGCAGATGGAGTGCATTTGTGTACAGGAGT	1080
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RESULT 4
BT020366
LOCUS
DEFINITION
ACCESSION
VERSION
BT020366.1 GI:56382004
FLI CDNA.
Arabisopsis thaliana (thale cress)
Arabisopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1128)
Kim, C.J., Chen, H., Cheuk, R., Shinn, P. and Ecker, J.R.
Arabisopsis ORF clones
Unpublished
2 (bases 1 to 1128)
Kim, C.J., Chen, H., Cheuk, R., Shinn, P. and Ecker, J.R.
Direct Submission
Submitted (04-DEC-2004) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA
The discrepancy does not affect the protein sequence.
Possible splice variant.
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Location/Qualifiers
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ORIGIN
Query Match 68.4%; Score 1113.8; DB 15; Length 1128;
Best Local Similarity 99.8%; Pred. No. 8.6e-308;
Matches 1115; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 208 ATGCTGTCTCCGAGCTCAAGAACCCGACCGCTCGCTACGAGACCGTGTAAATACCTC 267
DB 1 ATGCTGTCTCCGAGCTCAAGAACCCGACCGCTCGCTACGAGACCGTGTAAATACCTC 60

QY 268 CGTGACAGCTTAGACAGAGACCGCTCCAGCTCCTCGATACCGATGTGGCGAGTATCA 327
DB 61 CGTGACAGCTTAGACAGAGACCGCTCCAGCTCCTCGATACCGATGTGGCGAGTATCA 120

QY 328 GCGGCGCAGGACGTACTCGGCTGAGCTTCGGGCAACCGATCTGGTTGTCCTACT 387
DB 121 GCGGCGCAGGACGTACTCGGCTGAGCTTCGGGCAACCGATCTGGTTGTCCTACT 180

QY 388 CTTTCAGGACACACCGGAAAGGTTTATTTCATTAGATTGGACACCGGAGAACCGGATT 447
DB 181 CTTTCAGGACACACCGGAAAGGTTTATTTCATTAGATTGGACACCGGAGAACCGGATT 240

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QY 448 GTCAGTGCATCTCAAGATGGGAGATTAAATCGTGTGGAAATCTCTAAACGAGTCAGAAAAC 507
DB 241 GTCAGTGCATCTCAAGATGGGAGATTAAATCGTGTGGAAATCTCTAAACGAGTCAGAAAAC 300
QY 508 CATGCTATTAAACTCCCTTGTGCAATGGTATTATGATGCTTCTCTCCAAATGGTCAG 567
DB 301 CATGCTATTAAACTCCCTTGTGCAATGGTATTATGATGCTTCTCTCCAAATGGTCAG 360
QY 568 TCGGTTGGCTGTGGATTTAGACAGATGATGTTCTATCTTTAGCTTACGCTCAACGGG 627
DB 361 TCGGTTGGCTGTGGATTTAGACAGATGATGTTCTATCTTTAGCTTACGCTCAACGGG 420
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DB 421 GACAGGATGAACGTGTACCGGTTTCAAGATGCTCACTGTGTACAGGGGATATGTTTCG 480
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project).
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VERSION
AL023094.2 GI:5678625
SOURCE
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Arabisopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

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VERSION AL161585.2 GI:7270366  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana  
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
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3 (bases 109690 to 195921)  
Terry N., Ardiles W., Buysschaert C., Dasseville R., De Clerck R., De Keyser A., Rouze P., Van Den Daele H., Villarroel R., Gielen J., Van Montagu M., Mewes H.W., Lemcke K. and Mayer K.F.X. Unpublished  
4 (bases 1 to 195921)  
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Direct Submission  
Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de, project coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk  
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ this fragment has an overlap with ATCHRIV80 at the 5' end and an overlap with ATCHRIV82 at the 3' end.  
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Db	122820	ACGATAAAACGCTACTA	122804

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AF170921  
LOCUS  
DEFINITION  
ACCESSION  
VERSION

KEYWORDS	Pisum sativum (pea)	Db	471	TGATGGGATGGGAATCTAATATGTTTACGGATGCTTAGTGGAATAGAGTATGTTTC	530
SOURCE	Pisum sativum	Qy	687	GTGCTGTCAGTATGTCCTCAATAGGATGCCACTTATACACAGTTCAGGTGATCAAC	746
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.	Db	531	ATCTTGTGAGTATGTTCCAGGTGAAGACACTCACTTAATCACTGTTTCTGGAGATCAGAC	590
REFERENCE	1 (bases 1 to 1526)	Qy	747	TTGTATCTTATGGGATGTAACCTGCTCTCAAACTCTGTTTTTGGCGTGAATTTCA	806
AUTHORS	Lapik, Y.R. and Kaufman, L.S.	Db	591	ATGTTGTTTATGGGATATTTACTCTGCTTTAGAACATCTGTTTTTGGAGCGAGTTTCA	650
TITLE	Cloning of cDNA encoding pea G protein beta subunit	Qy	807	GTCTGGACATACCTGCTGATGTAAGCGTCTCAATCAGTGGATCAAAACCAACTGGTT	866
REFERENCE	2 (bases 1 to 1526)	Db	651	GTCTGGACATACCTGCTGATGTAAGCGTCTCAATCAGTGGATCAAAACCAACTGGTT	710
AUTHORS	Lapik, Y.R. and Kaufman, L.S.	Qy	867	TATATCTGTTTCATGCGGATCCACAGACCGTGTGGGACACTGCTGTCGAAGCCGAGC	926
TITLE	Direct Submission	Db	711	TGTATCTGTTTCTGCGATGCGACTGCCAGATTTGGGACACTGCTGTTGGCAAGTCGAGC	770
JOURNAL	Submitted (21-JUL-1999) Biological Sciences, University of Illinois at Chicago, 900 S. Ashland, Chicago, IL 60607, USA	Qy	927	AGTGGTACCTTTCATGCTCAGGAGGAGATGTTAATACGGTCAAGTCTTTCGGATGG	986
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**AUTHORS** Lein, W. **Direct** Submission  
**TITLE** Submitted (04-FEB-1997) Lein W., Institut fuer Pflanzen-genetik und  
**JOURNAL** Kulturpflanzenforschung, Molecular Cell Biology, Correnstrasse 3,  
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DEFINITION
ACCESSION Z84821
VERSION beta subunit; g protein.
KEYWORDS Nicotiana tabacum (common tobacco)
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REFERENCE 1 (bases 1 to 1434)
AUTHORS Lein, W. and Saalbach, G.
TITLE Characterization of G-protein function in plants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1434)
AUTHORS Lein, W.
TITLE Direct Submission
SUBMITTED (04-FEB-1997) Lein W., Institut fuer Pflanzen-genetik und
Kulturpflanzenforschung, Molecular Cell Biology, Corrensstrasse 3,
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JOURNAL		Biochim. Biophys. Acta 1491 (1-3), 143-160 (2000)	
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JOURNAL		Submitted (18-NOV-1996) C.S. Kaydamov, Institute of Plant Genetics, Molecular Genetics, Serology Group, Corrensestrae 3, Sachsen-Anhalt, Gatersleben, 06466, FRG	
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QY 1047 TCACCACTCCAGGT---CTATCAGCCACATGTTGTGTGTGAGAACGGACCTGTACCTC 1103
DB 963 ACACCAAGCTGCAAGTGTACTACAGCCGATGTTGTGTGTGTATCCCTCATGTGACTTC 1022
QY 1104 CATTCGATCTCTGTGTCAGGAGACTCTTTTTCGCTGTATGCGAGCAACACACTTG 1163
DB 1023 CATGGCAATTTCTATCTCAGGCGCTCTTCTCTTGTGCGGTACTC---AAATGGTGATG 1079
QY 1164 CTACGTTTGGGATPACCTCTTGGGAGAGTTGTATTGGATTTGGGATTTACAGCAGGATTC 1223
DB 1080 TTATGTGTGGACACCTATTAGCAAGGTGGTCTTAACCTTGGGAGGAGTTCAAACTC 1139
QY 1224 ACACGGAATAGAAATAGCTGTTTGGGTTGTGACAGATGGAAGTGCATTTGTGACAGG 1283
DB 1140 TCATGAAGSSGGATAAGTTGCTTGGACTGTGAGCTGTGAGTGGGAGSSCCTTATGTACAGG 1199
QY 1284 AGCTTCGGATTTCAAACTTAAAGATATGGGCTTTTGGAGGACACAGCAGAGTGTATTTGAA 1342
DB 1200 AGTTGGGATACAAACCTGAAGATTTGGGCTTTTGGAGGACACAGAGTGTATCTGAA 1258
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RESULT 12

AF414114

LOCUS AF414114 1540 bp mRNA linear PLN 30-APR-2002

DEFINITION Solanum tuberosum G protein beta subunit 2 (GB2) mRNA, complete

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AF414114  
AF414114.1 GI:15778631

Solanum tuberosum (potato)

Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamiales; Solanales; Solanaceae; Solanum.

1 (bases 1 to 1540)

Kang, S.G., Lee, H.J., Park, E.H. and Suh, S.G.

Molecular cloning and characterization of cDNAs encoding  
heterotrimeric G protein alpha and beta subunits from potato  
(Solanum tuberosum L.)

Mol. Cells 13 (1), 99-106 (2002)

11911481

2 (bases 1 to 1540)

Kang, S.-G. and Lee, H.-J.

Direct Submission

Submitted (27-AUG-2001) Institute of Biotechnology, Yeungnam

University, Kyongsan 712-749, Kyongsan 712-749, Korea

Location/Qualifiers

1..1540

/organism="Solanum tuberosum"

/mol\_type="mRNA"

/db\_xref="taxon:4113"

1..1540

/gene="GB2"

/gene="GB2"

/codon\_start=1

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/db\_xref="GI:15778632"

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LFVSGSCDTHLMDTRVSAQRTHFHGSDVTVTFKFPDGNRFGTSGDSCRLFD  
IRTGQVQNPQPHGDGDIPIHTSIASISGRIILFVYSGNDVYWDLLAKVNLV  
SVQNSHEGRISCLGLSDGSALCTGSMWNTLKIWAFGGHRSVI"

ORIGIN

Query Match 39.4%; Score 642.4; DB 15; Length 1540;

Best Local Similarity 73.9%; Pred. No. 1.6e-172;

Matches 843; Conservative 0; Mismatches 291; Indels 6; Gaps 2;

QY 205 GGAATGTCGTCTCGAGCTCAAGAACGCCACGCCGCTCGCTACGGAGACCGCTTAATAAC 264  
DB 93 GAAATGTCAGTTGCGAGCTGAAAGCGGCACATGGCGCTACACAGACTGTAATGAT 152  
QY 265 CTCCTGACACGAGCTTAGACAGAGACCGCTCCAGCTCTCGATACCGATGTGCGGAGGTAT 324  
DB 153 CTCCTGAAAACTTAAAGCAGAGCGCTCTCCAATTAATCTACACAGATGTTCTCGGTAT 212  
QY 325 TCAGCGCGCAAGGACGTACTCGGTGAGCTTCGGAGCAACGGATCTGGTTTGTGTCT 384  
DB 213 GCAAGAGCGCAGGTAAGAACTCCGGTAACGTTCCGCCCAACAGATCTAGTTTGTGTAGG 272  
QY 385 ACTCTTCAGGGACACACCGGAAGGTTTATTCTATTAGATTGGACACCGGAGGAGAACCGG 444  
DB 273 ATCTGCAAGGACACATGGAAGGCTTATTCTACCTGAGCTGACCTCTGAAAAAATCTGT 332  
QY 445 ATTTGTCAGTGCATCTCAAGATGGGAGATTAATCGTGTGGAATGCTCTAACGAGTCAGAAA 504  
DB 333 ATAGTCAGTGCATCCCAAGATGTAGATTAAATAGTGTGGAATGCTCTCAAGCCAGAAA 392  
QY 505 ACTCATGCTATTAAATCTCCCTTGTGCAATGGTTATGACATGTGCTTCTCTCAAAATGTT 564  
DB 393 ACCCATGCAATTAAGCTTCCATGTGCTGGTTATGACCTGTGCTCTCTCTAGTGA 452  
QY 565 CAGTCGGTTCCTGCTGGTGTAGACAGTGTATGTTCTTATCTTTAGCTCTAGCTCAACG 624



Db 453 CAGTCTGTTGCTTGCGGCGCTTGACAGTGCCTGCTCTATCTTCAACTTAATTCACCA 512

QY 625 GCGGACAAGAGTGAACCTGTACCGTTTCAAGAAATGCTCACTGTGTCACAGGGGATATGTT 684

Db 513 ATTGATAGGATGGATCCATCCAGTATCGAGATGCTTAGTGGCATAAGGGGTATGTG 572

QY 685 TCGTGTCTCAGTATGTCCTCAAAAGAGGATGCCACCTTATCACCAGTTCAGGTGATCAA 744

Db 573 TCTTCGTGTAGTATGTTCCGGATGAGGATATCACTCACTTAATAGTATGTTCTGGTGATCAA 632

QY 745 ACTTGATCTTATGGATGTAATCTGCTCAAAAACCTCTGTTTGGGGGTGAATTT 804

Db 633 ACATGTGTACTTTGGGATATAACTACTGCGCTTAAGAACTTCTGTGTTGGAGGTGAGTTT 692

QY 805 CAGTCTGACATATCTGTGATGTAATAGCGTCTCAATCAGTGGATCAAAACCCAACTGG 864

Db 693 CAATCTGGGCACATCTGACAGATGATCAAGTGTCTCAATTAGTTTCACTTAACCCCAACTA 752

QY 865 TTTATATCTGTTGATCGATTCACACAGCGTTGTGGGACACTGCTGCTGCAAGCCGA 924

Db 753 TTTGTGTCTGGTCTGTGACACAACTCTCGACTGTGGGACACCCGAGTTGCTAGTCTGA 812

QY 925 GCAGTGCCTACCTTTCATGGTTCACGAGGAGATGTTAATACGCTCAAGTCTTTCCGGAT 984

Db 813 GCTCAACGAACATTTATGGAACGAGAGTATGTTACTCTGTAAAGTCTTCCCTGAC 872

QY 985 GGTATAGATTTGGGACTGAGATCAGACGATGAAACATGACGCTGTATGACATAAGGACT 1044

Db 873 GGTATAGATTTGGAACTGGTTTCAGATGATGCGAGCTGCAGATTAATTTGACATAGGACT 932

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Db 933 GAACACCACTGCAAGTATACAAACCAACCGCATGTTGCGGTGACATCCCTCATGTGACT 992

QY 1102 TCCATTGCAATCTCTGTGTGAGGAGACTTCTTTTCGCTGCTATGCGAGCAACAACT 1161

Db 993 TCCATTGCAATTTCTATCTCAGCGCTCTTCTTTGTCGGGTACTC---TAATGGTAT 1049

QY 1162 TGCTACGTTTGGATACCTCTTGGGAGAGGTTGATTTGGATTTGGGATTAACAGCAGAT 1221

Db 1050 TGTACGTTGGGACACCTTATTAGCAAGGTGGTCTTAACATTAGGATCAGTTCAAAAC 1109

QY 1222 TCACACAGGAATAGATTAAGCTGTTGGGTTGTCAGCAGATGGAAGTGCAATGGTATCA 1281

Db 1110 TCTCATGAGCGGCAATAGTTGTTCTGGACTGTGAGCTGATGGAAGTGCCTTATGTACA 1169

QY 1282 GGAAGTTGGGATTTCAAACTTAAAGATATGGCGTTTGGAGGACACAGGAGATGATTTGA 1341

Db 1170 GGAAGTTGGGATACAACTGAGATTTGGGCTTTTGGAGGACACAGAAAGTGTGATCTGA 1229

RESULT 13

NTGPRBTBET 1560 bp mRNA linear PLN 18-APR-2005

LOCUS N.tabacum mRNA for G protein, beta subunit.

DEFINITION X98161

ACCESSION X98161.1 GI:1360091

VERSION cytoplasmic; G-protein beta subunit; signal transduction.

KEYWORDS Nicotiana tabacum (common tobacco)

SOURCE Nicotiana tabacum

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE 1

AUTHORS Kunesov,V.V. and Oelmuehler,R.

TITLE Isolation and characterization of cDNAs encoding the subunit beta of heterotrimeric G proteins from N. tabacum (Accession No. X98161) (PCR96-048)

JOURNAL Plant Physiol. 111, 948-948 (1996)

REFERENCE 2 (bases 1 to 1560)

AUTHORS Oelmuehler,R.

TITLE Direct Submission

JOURNAL Submitted (28-MAY-1996) R. Oelmuehler, Botanisches Institut der

Ludwig-Maximilians-Universitaet, Menzingerstr 67, 80638 Muenchen, FRG

Ref [3]: Plant Gene Register PCR96-048 (1996).

Location/Qualifiers

source 1..1560

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/mol\_type="mRNA"

/cultivar="Samsun NN"

/db\_xref="taxon:4097"

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/dev\_stage="seedlings"

120..1247

/function="signal transduction"

/note="beta subunit localized in cytoplasm"

/codon\_start=1

/product="G protein"

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/db\_xref="GI:1360092"

/db\_xref="GOA:Q40507"

/db\_xref="InterPro:IPR001632"

/db\_xref="InterPro:IPR001680"

/db\_xref="InterPro:IPR011046"

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ORIGIN

Query Match 39 4%; Score 641.2; DB 15; Length 1560;

Best Local Similarity 74.5%; Pred. No. 3.6e-12; Indels 7; Gaps 3;

Matches 848; Conservative 0; Mismatches 283;

QY 207 AATGTCTGTCTCCGAGCTCAAAGAACCGCCACGCGTCGCTACGGAGACCGTTAATAACCT 266

Db 119 AATGTAGTGACAGAGCTGAAAGAGCGCATATGCGCGCTACACAGACTGTAAGTGATCT 178

QY 267 CCGTGACCGAGCTTAGACAGAGACGCTCCAGCTCCTCGATACCGATGTGGCAGGATATTC 326

Db 179 CCGTGAAGAACTTAAGCAGAGAGCTCTCCAATTAATCTGCACACTGATGTTCTGGATATGC 238

QY 327 AGCGCGCAGAGGACGTACTCGGTGAGCTTCGGAGCAACGGATCTGTTGTTGTCGTAC 386

Db 239 AAGTCCGAGGTAAACTCCGGTCACCTTTGGCCCCAACAGATCTGGTTTGTGTAGGAT 298

QY 387 TCTTCAGGACACACCGGAAAGTTTATTCAATTAGATTGGACACCGGAGAGAACCGGAT 446

Db 299 CTTCAAGGACACACTGAAAGGTATATTCACTGATTGGACTCCAGAAAGAAATCGTAT 358

QY 447 TGTCAGTGCATCTCAAGATGGAGATTAATCGTGTGGAATGCTCTTAAGAGTCAAGAAAC 506

Db 359 AGTCAGTGCATCCCAAGATGGCAGATTAATAGTGTGGAATGCTCTCAAGCCAGAAAC 418

QY 507 TCATGCTATTAACTCCCTTGTGCATGGTTATACATGTCCTTCTCCAAATGGTCA 566

Db 419 CCATGCAATTAAGCTTCCTGTTGTTATGACCTGCGCCCTTCTCTCTAGTGGGCA 478

QY 567 GTCGGTTGCGTGTGGATTAGACAGTGTATGTTCTATCTTTAGCCCTTACTCAACGCC 626

Db 479 GTCTGTTGCCCTGCGGTGCGCTTGACAGTGTCTGCTCTATCTACAACTTAAATTCGCCAAT 538

QY 627 GGACAGAGTGAAGTGTACCGGTTTCAAGATGCTCAAGATGCTCACTGCTCAGAGGATATGTTTC 686

Db 539 CGATAAGGATGGGAACCATCTCTGTATCAAGAAATCTTAGTGGGATAGGGGTATGTGTC 598

QY 687 GTGCTGTCAGTATCTCCCAATAGGATGCCACCTTATCACCAGTTTCAGGTGATCAAAAC 746

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Db      599 TTCCTGTCAATATGTTCCAGATGAGGATACTCACCTAATAACTAGTTCGTGGTGATCAAC 558
Qy      747 TTGTATCTTATGGGATGTAATCTACTGGTCTCAAACTTCTGTTTTTGGCGGTGAATTTCA 806
Db      659 ATGTGTCTCTTTGGGATATAAATACTACTGGTCTAAGAACTTCTGTCTTTGGAGGTGAGTTTCA 718
Qy      807 GTCCTGGACATAGTGTGATGTAAGTCTCAATCAGTGTGATCAAAACCCAACTGGTT 866
Db      719 ATCCGGGACACTGACAGATGTAAAGTGTCTCAATTTAGTTTCAATCAACCCAGACTGTT 778
Qy      867 TATATCTGTTTCATGCGATTCACAGCAGCGTTGTGGGACACTCGTGTCTGCAAGCCGAGC 926
Db      779 TGTATCTGGTCTCTGTGACAACTGCTCGACTGTGGGACACCGAGTTGCTAGTCGAGC 838
Qy      927 AGTGGCTACTTTCATGTTGTCAGAGGAGATGTTAATACGGTCAAGTTCTTTCCGGATGG 986
Db      839 TCAACGAACATTTTATGGTCACGAGGAGATGTTAATACTGTAAAGTTCTTCCCTGATGG 898
Qy      987 GTATAGATTGGGACTGGATCAGACGATGGAATCGACGCTGTATGATCAATAGGACTGG 1046
Db      899 TAATAGATTGGAACCTGGTTTCAGAGGATGGAACCTGACAGATTATTTGACATTAGGACTGG 958
Qy      1047 TCACCAACTCCAGT---CTATCAGCCACATGCTGATGCTGAGAACCGGACCTGTCACTTC 1103
Db      959 ACACGAGCTGCAAGTGTACTACAGCCGCAATGGTGTATGATATCCCTCATGTGACTTC 1018
Qy      1104 CATTCGATCTCTGTCTCAGGAGACTTCTTTTCGCTGGCTATGCGAGCAACAACTG 1163
Db      1019 CATGGCAATTTCTATCTCAGGCGCTCTTCTCTTTGTCGGATACTC---AAATGGTGATTG 1075
Qy      1164 CTACGTTTGGGATACCTCTGGGAGAGTTGTATTTGGATTGGGATTACAGCAGATTTC 1223
Db      1076 TTATGTGTGGGACACCTATTAGCAAGGTGTCCTAATCTTGGGAGGAGTTCAAAACTC 1135
Qy      1224 ACACAGGAATAGAAATAGCTTTTGGGGTTGTGAGCAGATGGAAGTGCAATTGTGTACAG 1283
Db      1136 TCATGAAGGGCGAATAGTTGCTTGGGACTGTGAGTGTATGAGGCGCTTATGTACAGG 1195
Qy      1284 AAGTTGGGATTCAAATCTAAGANATGGCGTTTGGAGGACACAGAGAGTGAATTTGA 1341
Db      1196 AAGTTGGGATACAACTGAAGATTTGGGCTTTTGGAGG-GACAGAAAGTGTGATCTGA 1252

RESULT 14
STGB1GENE      1524 bp      mRNA      linear      PLN 18-APR-2005
LOCUS          S.tuberosum mRNA for beta 1 subunit of heterotrimeric G-protein.
DEFINITION     X87837
ACCESSION      X87837.1 GI:1771733
VERSION        beta-1 subunit; g protein; gb1 gene; GB1 protein.
KEYWORDS       Solanum tuberosum (potato)
SOURCE         Solanum tuberosum
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE      1
AUTHORS        Provart,N.J., Ma,H., Willmitzer,L. and Mueller-Roeber,B.
TITLE          Cloning of 2 subunits of a G-protein from a potato guard cell cDNA
                bank
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 1524)
AUTHORS        Provart,N.J.
TITLE          Direct Submission
JOURNAL        Submitted (07-JUN-1995) N.J. Provart, Inst. fuer Genbiologische
                Forschung GmbH, Ihnestrasse 63, 14195 Berlin, FRG
FEATURES       source
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/dev_stage="8 weeks"
1..1524
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49..1182
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/db_xref="GOA:P93563"
/db_xref="InterPro:IPR001632"
/db_xref="InterPro:IPR001680"
/db_xref="InterPro:IPR011046"
/db_xref="UniProt/Swiss-Prot:P93563"
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LFVSGSDITARKLMDIRVASRAQRTTFHGHSDVNTKFPDGNRRTGSDGSCRLFD
IRTGHLQVYNQPHGDDGDIPIHTSNMFIISGRLLFVGSNGSDCYVYDNTLLAKVLNLG
SVQNSHEGRISICLGLSADGSALCTGSWDTNLKIWAFGGHRSVV"

ORIGIN
Query Match      39.3%; Score 640.8; DB 15; Length 1524;
Best Local Similarity 73.9%; Pred. No. 4.6e-172;
Matches 842; Conservative 0; Mismatches 292; Indels 6; Gaps 2;

Qy      205 GGAATGTCTGTCTCCGAGCTCAAAGAACCCACGCGTCCGTACGAGACCGTTAATAAC 264
Db      46  GAAATGTCAATTTAAGCAGAACGCTCTCCAAATTAATCGACACAGATGTTCTGGGTAT 105
Qy      265 CTCCTGACCACTTAGACAGAGACGCTCCAGCTCTCGATACCGATCGGTGGAGGTAT 324
Db      106 CTCCTGAAAACTTAAGCAGAACGCTCTCCAAATTAATCGACACAGATGTTCTGGGTAT 165
Qy      325 TCAGCGGCGCAAGGAGTACTCGGTGAGCTTCGGAGCAACGGATCTGTTGTTTCGT 384
Db      166 GCAAGAGCAAGGTAAAGTCCGGTAACTTCGGCCCAACAGATCTAGTTTGTGTAGG 225
Qy      385 ACTCTTCAGGGACACACCGGAAAGTTTATTCAATAGATTGGACACCGGAGAGAACCGG 444
Db      226 ATCTTCAAGGACACACTGGAAGGTCTATTCTACGACTGGACTCTCGAAAAAATCGT 285
Qy      445 ATTGTGAGTGCATCTCAAGATCGGAGATTAATCGTGTGAATGCTCTAACGAGTCAGAA 504
Db      286 ATAGTCAGTGCATCCCAAGATGATAGATTAAATAGTGTGAATGCTCTCAAGCCAGAA 345
Qy      505 ACTCATGCTATTAAACTCCCTTGTGCATGGGTTATGACATGCTTCTCTCCAAATGTT 564
Db      346 ACCCATGCAATTAAGCTTCCATGTGCTGGGTTATGACCTGTGCTTCTCTCTAGTGA 405
Qy      565 CAGTGGTTGCTGTGTGCTGATTAGACAGTGTATGTTCTATCTTTAGCCTTAGCTCAACG 624
Db      406 CAGTCTGTTGCTTGTGGCGGCTTGACAGTGTCTGCTCTATCTTCAACTTAATTCACCA 465
Qy      625 GGGGCAAGAGTGGAACTGTACCGGTTTCAAGAATGCTCACTGGTCACAGGGGATATGTT 684
Db      466 ATCGATAAGATGGGATCCATCCAGTATCGAAATGCTTTAGTGGGCATAAGGGGTATGTG 525
Qy      685 TCGTGTCTGATATGTCCCAATAGGATGCCACCTTATCCACAGTTTCAGTGTATCA 744
Db      526 TCTTCGTGTGATGTTCCCGATGAGGATACCTACCTAATAACTAGTTCTGTGTATCAA 585
Qy      745 ACTTGTATCTTATGGGATGTAATCTACTGTCTCAAACTCTCTGTTTTGCGGTGAATTT 804
Db      586 ACATGTGATCTTTGGGATATACTACTGGCCTTAAGAACTTCTGTGTTTGGAGTGTAGTTT 645
Qy      805 CAGTCTGGACATCTCTGTATGATCAAGCGTCTCAATCAGTGGATCAAAACCAACTGG 864
Db      646 CAATCTGGGCACATCTGACATGTTAATAGTGTCTCAATTAGTTTCACTTAACCCCAACTG 705
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706 TTGTGTCTGGGTCCTGTGACACAACTGCTCGACTGTGGGACACCCCGAGTTGCTAGTCGA 765

QY GCAGTGGCGTACCTTTCATGTTGTCACAGGAGAGATTTAATACGTCACGTTCTTTCCGGAT 984
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766 GCTCAACGAACTTTCATGCGACAGAGAGTGNATTAATCTGTANAGTTCTTCCTGAC 825

QY GGGTATAGATTGGAGCTGGATCAGACGATGGAACATCAGGCTGTATGACATAGGACT 1044
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826 GGTAAATAGATTGGAACTGGTTTCAGATGATGGAAGCTCAGATTATTTGACATTAGGACT 885

QY GGTCAACCACTCCAGGT---CTATCAGCCACATGCTGATGTGAGAACGGACCTGTCAAC 1101
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886 GGACACCAAGCTGCAAGTATACAACCAACCGCATGGTGACGCTCATCTCATGTGACT 945

QY TCCATTGCAATCTCTGTGTGAGGAGACTTCTTTTCGCTGGCTATGCGAGCAACAACACT 1161
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946 TCCATGGCAATTTCTATCTCAGCCGCTCTTCTTTGCGGGTACTC---TAATGGTGAT 1002

QY TGCTACGTTTGGGATPACCTCTTGGGAGAGTTGATTTGGATTGCGGATTAACAGCAGGAT 1221
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1003 TGTACGTGTGGGACACCTATTAGCAAGGTGGTCTTAAACTTAGGATCAGTTCAAAC 1062

QY TCACACAGGAATAGAAATAGCTGTTTGGGTTGTTCAGCAGATGGAAGTGCAATTGTGTACA 1281
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1063 TCTCATGAAGGCGGAATAAGTTGTCTGGGACTGTTCAGCTGACGGAAGTGCCCTTATGTACA 1122

QY GGAAGTTGGGATTCAAATCTTAAAGATATGGGCTTTGGGAGACACAGGAGAGTATTGA 1341
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1123 GGAAGTTGGGATACAACTGNAGATTGGGCTTTGGAGGACACAGAAGTGTGTCTGA 1182

RESULT 15
AF145976 1611 bp mRNA linear PLN 01-JUN-1999
LOCUS Pium sativum G protein beta subunit mRNA, complete cds.
DEFINITION AF145976
ACCESSION AF145976
VERSION AF145976.1 GI:4929351
KEYWORDS
SOURCE
ORGANISM
Pium sativum (pea)
Pium sativum
Pium sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Pium.
1 (bases 1 to 1611)
Wu, Y. and Tuteja, N.
Isolation and characterization of G protein from pea
Unpublished
2 (bases 1 to 1611)
Wu, Y. and Tuteja, N.
Direct Submission
Submitted (26-APR-1999) Plant Molecular Biology, ICGEB-New Delhi,
Aruna Asaf Ali Marg, New Delhi 110067, India
FEATURES
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/mol_type="mRNA"
/db_xref="taxon:3888"
144..1277
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various transmembrane signaling systems"
/note="contains 7 WD repetitive region"
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/protein_id="AAD33959.1"
/db_xref="GI:4929352"
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IKLPCAWMTCAFSPGTVACGLDSCVSI.FNLNSPLDRGNLNVSMLSGHKYVS
SCQVVPGRDHLITGSGDQTCVMDITTLGLATSVLGEFQSGHTADVLISINGSNK
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ORIGIN
Query Match 39,38; Score 640.6; DB 15; Length 1611;
Best Local Similarity 73.5%; Pred. No. 5.3e-172; Indels 6; Gaps 2;
Matches 846; Conservative 0; Mismatches 239;
QY 194 AGTCTGATCCCGGAATCTGTCTCCGAGCTCAAAGAACCCACGCGTCCGTACGGAGA 253
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QY 254 CCGTTAATACTTCCTGTCAGCTTAGACAGAGACGCTCCAGCTCTCTGATACCGATG 313
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
190 CGGTTAACAATCTCAGAGAACGATTGACAGAGACCGGCTTTCTTTGCTGATACAGATA 249

QY 314 TGGCGAGGATTTACAGCGCGCAAGGACGTACTCGGGTGAGCTTCGGAGCAACGATCTGG 373
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250 TTGCTGGATATGCTAGGTCTCAAGGTAGAGTCTCTGTACTCTTTTGGTCCCACTGATATTC 309

QY 374 TTTGTTGTCTGACTCTTTCAGGACACACCCGAAAGGTTTATTCATTAGATTGGACACCG 433
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QY 494 CGAGTCAGAAAACTCATGCTATTAAACCTCCCTCTGTGATGGTTTATGACATGTCTTTCT 553
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QY 554 CTCCAAATGGTTCAGTCCGTTGCGGTGTGGATTAGACAGTGTATGTTCTATTAGCC 613
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490 CACCAACTGGTCAATCTGTTGCTTGTGGGSCCTTGACAGTGTGTTGCTCTATTATTCATC 549

QY 614 TTACTCAACGCGCGGACAGAGATGGAATGTACCGGTTTCAAGAACTGCTCACTGTCACA 673
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550 TTAATCTCCACTCGATAGGATGGGAATCTAAATGTTTTCACGGATGCTTAGTGACATA 609

QY 674 GGGGATATGTTTCGTGCTGTCAGTATGTCCTCAAAATGAGGATGCCCTTATACCAAGTT 733
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610 AAGTTATGTTTCACTTGTGTCAGTATGTTCCAGGTGAAGACACTCACTTAATCACTGGTT 669

QY 734 CAGGTGATCAAACTTGTATCTTATGGGATGTAACTACTGTGCTCTCAAACTTCTGTTTTG 793
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QY 794 CGGTGAATTTTCAGTCTGGACATACCTGCTGATGTACTAAGGCTCTCAATCAGTGGATCAA 853
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QY 1034 ACATAAGGACTGTGTCACCACTCCAGTCT---ATCAGCCACATGCTGATGCTGAGAACG 1090
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QY 1091 GACCTGTCACTCCATTCGATTTCTCTGTGTCAGGAGACTTCTTTTCGCTGGCTATCGGA 1150
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Db      1087 CAAATGGTGATTGCTATGTTGGGATACCTTATTGGCTAAGGTGGTCTTGAATCTAGGAT 1146
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Db      1147 CTCCTTCAAAACTCTCATGAGGSCAGGATCACCTGTTTGGGTATGTCCTGATGGAAGCG 1206
Qy      1271 CATTGTGTACAGGAAGTTGGGATTCAAATCTAAAGATATGGCCGTTTGGAGGACACAGGA 1330
Db      1207 CTTTATGTACAGGAAGTTGGGACACAAATTTAAAGATATGGGCAATTGGAGGGCATAGGA 1266
Qy      1331 GAGTGATTGA 1341
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Search completed: December 28, 2005, 17:47:36  
 Job time : 8039 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: December 28, 2005, 08:46:01 ; Search time 943 Seconds  
(without alignments)  
11513.027 Million cell updates/sec

Title: US-10-602-898A-1  
Perfect score: 1629  
Sequence: 1 cctgacgtacacgtgttg.....cagaagataaaacgctacta 1629

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21.\*  
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2: Geneseqn1990s.\*  
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9: Geneseqn2003bs.\*  
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12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	1629	100.0	1629	12	ADH78721	Adh78721 Arabidops
2	1439.4	88.4	1465	3	AAC45984	Aac45984 Arabidops
3	1434.6	88.1	1467	3	AAC37381	Aac37381 Arabidops
4	1132.4	69.5	1134	12	ADN72944	Adn72944 Thale cre
5	728.6	44.7	802	6	ABN99039	Abn99039 Arabidops
6	661.6	40.6	1526	12	ADH78737	Adh78737 Pea AGB1
7	656.4	40.3	1430	12	ADH78735	Adh78735 Tobacco A
8	654.8	40.2	1600	12	ADH78729	Adh78729 Tobacco A
9	651	40.0	1434	12	ADH78733	Adh78733 Tobacco A
10	647.4	39.7	1676	14	AE26929	Aeb26929 Pinus rad
11	642.4	39.4	1540	12	ADH78725	Adh78725 Potato AG
12	641.2	39.4	1560	12	ADH78731	Adh78731 Tobacco A
13	640.8	39.3	1524	12	ADH78727	Adh78727 Potato AG
14	640.6	39.3	1611	12	ADH78739	Adh78739 Pea AGB1
15	637.6	39.1	693	3	AAC44600	Aac44600 Arabidops
16	576.4	35.4	1664	12	ADH78743	Adm78743 Rice AGB1
17	558.8	34.3	1480	12	ADM47702	Adm47702 Polynucle
18	558.8	34.3	1671	12	ADH78745	Adh78745 Maize AGB
19	558.2	34.3	1924	14	AEB27029	Aeb27029 Pinus rad

20	551.8	33.9	1470	12	ADH78741	Adh78741 Wild oat
21	545	33.5	756	3	AAC43814	Aac43814 Arabidops
22	529.8	32.5	1123	13	ADX7418	Adx7418 Plant ful
23	433	26.6	984	12	ADJ39635	Adj39635 Plant cdn
24	322.4	19.8	594	12	ADJ44713	Adj44713 Plant cdn
25	222.2	13.6	786	3	AAC51866	Aac51866 Arabidops
26	142	8.7	2208	12	ADG73724	Adg73724 Aspergill
27	138	8.5	1457	4	AAI59460	Aai59460 Human pol
28	138	8.5	2567	4	AHI14842	Ahi14842 Human cdn
29	138	8.5	2567	10	ADD18943	Add18943 Human dis
30	138	8.5	2567	13	ADR24374	Adr24374 Breast ca
31	138	8.5	2923	10	ADD12690	Add12690 Human cdn
32	136.6	8.4	1023	9	ADA02731	Ada02731 Mouse Gnb
33	136.6	8.4	1023	10	ADB72469	Adb72469 Mouse Gnb
34	136.6	8.4	1023	10	ADE95979	Ade95979 Mouse Gnb
35	136.6	8.4	1410	6	ABI99519	Abi99519 Mouse isc
36	136.6	8.4	1410	9	ADA02730	Ada02730 Mouse Gnb
37	136.6	8.4	1410	10	ADB72468	Adb72468 Mouse Gnb
38	136.6	8.4	1410	10	ADE95978	Ade95978 Mouse DNA
39	136.6	8.4	1410	10	ABV75223	Abv75223 Murine GN
40	135	8.3	2837	10	ADB58549	Adb58549 Toxicity-
41	135	8.3	2837	10	ADB53156	Adb53156 Primary r
42	135	8.3	2837	10	ABT42151	Abt42151 Toxicity
43	135	8.3	2837	13	ADV41343	Adv41343 Rat card1
44	131	8.0	669	12	ADJ43948	Adj43948 Plant cdn
45	130	8.0	1520	3	AAA74590	Aaa74590 Rat Taste

ALIGNMENTS

RESULT 1

ADH78721  
ID ADH78721 standard; DNA; 1629 BP.

AC ADH78721;

DT 22-APR-2004 (first entry)

XX Arabidopsis thaliana AGB1 gene, SEQ ID 1.

XX Plant; agronomic trait; flowering; fruit yield; seed yield; root biomass;  
XX seed size; seed shape; stem branch number; plant size; gene; db;  
XX GPA.

OS Arabidopsis thaliana.

PN WO2004003146-A2.

PD 08-JAN-2004.

PF 24-JUN-2003; 2003WO-US020001.

PR 28-JUN-2002; 2002US-0392730P.

PR 05-FEB-2003; 2003US-0445208P.

XX (PARA-) PARADIGM GENETICS INC.  
XX (UYNC-) UNIV NORTH CAROLINA.

PI Boyes D, Davis K, Jones A, Ullah H, Chen J, Mulpuri R;  
PI Chatterjee A, Ward MP;

DR WPI; 2004-083031/08.

DR P-PSDB; ADH78722.

XX Altering a plant agronomic trait, useful for improving plant agronomic  
XX traits comprising regenerating plants having stably integrated expression  
XX cassette, where the regenerated plant has an altered agronomic trait.

XX Claim 4; SEQ ID NO 1; 180pp; English.

XX The present invention relates to a method for altering a plant agronomic  
XX trait selected from time to flowering, duration of flowering, fruit





XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 48488.  
XX KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
XX promoter; termination sequence; ss.  
XX OS Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-00301439.  
XX PR 25-FEB-1999; 99US-0121825P.  
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Qy	493	ACGAGTCAAGAAACTCATGCTATTAAACTCCCTTGTGATGGGTTATGACATGTGCTTTC	552
Db	494	ACGAGTCAAGAAACTCATGCTATTAAACTCCCTTGTGATGGGTTATGACATGTGCTTTC	553
Qy	553	TCTCAAAATGGTCAAGTCGGTTGCGTGTGGTGGATTAGACAGTGATGTTCTATTAGC	612
Db	554	TCTCAAAATGGTCAAGTCGGTTGCGTGTGGTGGATTAGACAGTGATGTTCTATTAGC	613
Qy	613	CTTAGCTCAACGCGGCAAGGATGGAACCTGTACCGGTTTCAAGAAATGCTCACTGGTCAC	672
Db	614	CTTAGCTCAACGCGGCAAGGATGGAACCTGTACCGGTTTCAAGAAATGCTCACTGGTCAC	673
Qy	673	AGGGATATGTTTCGTGCTGTCACTATGTCCCAAATGAGGATGCCCACTTTATCACCAGT	732
Db	674	AGGGATATGTTTCGTGCTGTCACTATGTCCCAAATGAGGATGCCCACTTTATCACCAGT	733
Qy	733	TCAGGTGATCAAACTTGATGTTCTTATGGGATGTAATCTACTGTCTCAAACTTCTGTTTT	792
Db	734	TCAGGTGATCAAACTTGATGTTCTTATGGGATGTAATCTACTGTCTCAAACTTCTGTTTT	793
Qy	793	GGCGTGAAATTTTCAGTCTGGACATCTGCTAGTCTTAAGCGCTCTCAATCAGTGGATCA	852
Db	794	GGCGTGAAATTTTCAGTCTGGACATCTGCTAGTCTTAAGCGCTCTCAATCAGTGGATCA	853
Qy	853	AACCCAAACTGGTTTATATCTGGTTTCATGCGATTCCACAGCACCGTTGTGGGACACTCGT	912
Db	854	AACCCAAACTGGTTTATATCTGGTTTCATGCGATTCCACAGCACCGTTGTGGGACACTCGT	913
Qy	913	GCTGCAAGCCGAGCAGTGCCTTTCATGCTGTCACGAGGAGATGTTAATACGGTCAAG	972
Db	914	GCTGCAAGCCGAGCAGTGCCTTTCATGCTGTCACGAGGAGATGTTAATACGGTCAAG	973
Qy	973	TTCTTTCCGGATGGTATAGATTTGGGACTGGAATGAGCAATGCAATGCAAGGCTGAT	1032
Db	974	TTCTTTCCGGATGGTATAGATTTGGGACTGGAATGAGCAATGCAATGCAAGGCTGAT	1033
Qy	1033	GACATAAGGACTGGTCCAACTCCAGGTCTATCAGCCACATGGTGTGAGAACCGA	1092
Db	1034	GACATAAGGACTGGTCCAACTCCAGGTCTATCAGCCACATGGTGTGAGAACCGA	1093
Qy	1093	CCTGTACCTCCATGCAATCTCTGTGTACGGGAGACTTCTTTTCGTGCGCTATGCGAGC	1152
Db	1094	CCTGTACCTCCATGCAATCTCTGTGTACGGGAGACTTCTTTTCGTGCGCTATGCGAGC	1153
Qy	1153	AACAACCTTGTCTACGTTTGGGATACCTCTTTGGGAGAGGTTGATTTGGGATTTA	1212
Db	1154	AACAACCTTGTCTACGTTTGGGATACCTCTTTGGGAGAGGTTGATTTGGGATTTA	1213
Qy	1213	CAGCAGGATTCACACAGGAATAGAAATAGCTGTTTGGGTTTGTGAGGATGGAAGTCA	1272
Db	1214	CAGCAGGATTCACACAGGAATAGAAATAGCTGTTTGGGTTTGTGAGGATGGAAGTCA	1273
Qy	1273	TTGTGTACAGGAAGTTGGGATTTCAATCTAAAGATATGGGCGTTTGGAGGACAGGAGA	1332
Db	1274	TTGTGTACAGGAAGTTGGGATTTCAATCTAAAGATATGGGCGTTTGGAGGACAGGAGA	1333
Qy	1333	GTGATTTTGAAGAACTTTAAACGAAAGTAGGAGTCACTCTCCAGTTGTTGCTTAATATA	1392
Db	1334	GTGATTTTGAAGAACTTTTAAAGTAGGAGTCACTCTCCAGTTGTTGCTTAATATA	1392

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QY 1393 TTCTGTAGTCGGAGTACAGGTTTCGGTTTGTGGAAGGTTTGGTTTGAATAGTGAGCT 1452
DB 1393 TTCTGTAGTCGGAGTACAGGTTTCGGTTTGTGGAAGGTTTGGTTTGAATAGTGAGCT 1452
QY 1453 GGTTAGAAGAAATT 1465
DB 1453 GGTTAGAAGAAATT 1465

RESULT 3
AAC37381
ID AAC37381 standard; DNA; 1467 BP.
XX AAC37381;
XX
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 17173.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
PR 05-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
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PR 14-MAY-1999; 99US-0134219P.
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PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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PR 10-JUN-1999; 99US-0138540P.
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PR 24-JUN-1999; 99US-0140695P.
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PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
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PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
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PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
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PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
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Db 841 CACCAACTCCAGGCTCTATCAGCCACATGGTATGTTGAGAACGGACCTGTACCTCCATT 900  
Qy 1108 GCATTCTCTGTCTAGGAGACTCTCTTTTCGCTGCTATGCCAGCAACAACACTTGTCTAC 1167  
Db 901 GCATTCTCTGTCTAGGAGACTCTCTTTTCGCTGCTATGCCAGCAACAACACTTGTCTAC 960  
Qy 1168 GTTTGGGATACCTCTTGGGAGAGGTTGTATTTGGATTTGGGATTTACAGCAGGATTCACAC 1227  
Db 961 GTTTGGGATACCTCTTGGGAGAGGTTGTATTTGGATTTGGGATTTACAGCAGGATTCACAC 1020  
Qy 1228 AGGATAGAAATAGCTGTTTGGGTTGTCAGCAGATGGAAGTGCATTTGTACAGGAAGT 1287  
Db 1021 AGGATAGAAATAGCTGTTTGGGTTGTCAGCAGATGGAAGTGCATTTGTACAGGAAGT 1080  
Qy 1288 TGGGATTCAAATCTAAAGATATGGCGTTTGGAGACACAGGAGAGTGAATTGA 1341  
Db 1081 TGGGATTCAAATCTAAAGATATGGCGTTTGGAGACACAGGAGAGTGAATTGA 1134

RESULT 5

ID ABN99039  
XX ABN99039 standard; DNA; 802 BP.  
AC ABN99039;  
XX  
DT 01-AUG-2002 (first entry)  
XX  
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 807.  
XX  
KW Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;  
KW disease; crop; thale cress; tolerance factor; insect; pathogen;  
KW nutrition; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
PN US200203281-A1.  
XX  
PD 21-FEB-2002.  
XX  
PF 26-JAN-2001; 2001US-00770445.  
XX  
PR 27-JAN-2000; 2000US-0178472P.  
XX

(GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHAW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
XX  
PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;  
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;  
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;  
PI Hurban P;  
XX  
DR WPI; 2002-403163/43.  
XX  
XX New Arabidopsis thaliana nucleic acid for identifying homologous genes,  
PT producing compositions that modulate the expression or function of its

PT encoded protein, and mapping functional regions of protein.  
XX  
PS Claim 1; SEQ ID NO 807; 49pp + Sequence Listing; English.  
XX  
CC The invention relates to an Arabidopsis thaliana nucleic acid (I)  
CC comprising a sequence capable of hybridising under stringent conditions  
CC to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),  
CC given in the specification or its fragment. A polypeptide (II) encoded by  
CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a  
CC genetically modified cell (IV) comprising an exogenous nucleic acid, is  
CC useful for screening a candidate agent for its biological effect. (I) is  
CC useful in identifying homologous or related genes, in producing  
CC compositions that modulate the expression or function of its encoded  
CC protein, mapping functional regions of the protein and in studying  
CC associated physiological pathways. (I) is also useful for the genetic  
CC manipulation of cells, particularly plant cells. (I) is also useful in  
CC screening assays of various plant strains to determine the strains that  
CC are best capable of withstanding a particular disease or environmental  
CC stress. (II) and (III) are useful for screening of biologically active  
CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical  
CC pathways. The screened agents are useful in improved methods of treating  
CC crops to prevent or treat disease. (II) are also useful in screening  
CC programs to identify agents that mimic or enhance the action of tolerance  
CC factors. Such agents are useful in improved methods of treating crops to  
CC enhance their tolerance to environmental stress. (I) is also useful for  
CC enhancing or inhibiting production of a biosynthetic product in a plant.  
CC (III) is useful for identifying other mediators that may induce  
CC expression of proteins of interest, for establishing the extent to which  
CC any specific insect and/or pathogen is responsible for damage to a  
CC particular plant, for identifying other mediators that enhance or induce  
CC tolerance to environmental stress, for identifying factors involved in  
CC biosynthetic pathways of nutritional, commercial, or medicinal value and  
CC for identifying productions of nutritional, commercial or medicinal  
CC value. (IV) is useful in the study of genetic function and regulation,  
CC for alteration of the cellular metabolism and for screening compounds  
CC that may affect the biological function of the gene or gene products.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPTO  
CC at seqdata.uspto.gov/sequence.html?docID=99909770445  
XX  
SQ Sequence 802 BP; 230 A; 133 C; 202 G; 227 T; 0 U; 10 Other;

Query Match 44.7%; Score 728.6; DB 6; Length 802;  
Best Local Similarity 95.5%; Pred. No. 2.2e-215;  
Matches 765; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

Qy 821 CTGATGTACTAAGCGTCTCAATCAGTGGATCAAAACCCAACTGGTTTATATCTGTTTCAT 880  
Db 1 CTGATGTACTAAGCGTCTC-ATCAGTGGATCAAAACCCAACTGGTTTATATCTGTTTCAT 59  
Qy 881 CGGATTCACAGCAGCGTTTGGGACACTCGTGTGCAAGCCGAGCGTGCCTACCTTTC 940  
Db 60 CGGATTCACAGCAGCGTTTGGGACACTCGTGTGCAAGCCGAGCGTGCCTACCTTTC 119  
Qy 941 ATGCTCAGGAGGAGATGTTAATACGTTCTTTCCGGATGGGTATAGATTGGGA 1000  
Db 120 ATGCTCAGGAGGAGATGTTAATACGTTCTTTCCGGATGGGTATAGATTGGGA 179  
Qy 1001 CTGGATCAGACGATGGAACATGCAAGCTGTATGACATAAGGACTGGTCACCACTCCAGG 1060  
Db 180 CTGGATCAGACGATGGAACATGCAAGCTGTATGACATAAGGACTGGTCACCACTCCAGG 239  
Qy 1061 TCTATCAGCCACATGGTGAATGGTGAGAACCGGACCTGTCCACTCCATTCCTCTGTGT 1120  
Db 240 TCTATCAGCCACATGGTGAATGGTGAGAACCGGACCTGTCCACTCCATTCCTCTGTGT 299  
Qy 1121 CAGGAGACTTCTTTTCGCTGGCTATGGGAGCAACACACTTGCTACGTTTGGGATACCC 1180  
Db 300 CAGGAGACTTCTTTTCGCTGGCTATGGGAGCAACACACTTGCTACGTTTGGGATACCTN 359  
Qy 1181 TCTTGGGAGAGGTTGTATTGGATTGGGATTACAGCAGGATTTCACAGGAAATAGATAA 1240  
Db 360 TCTTGGGAGAGGTTGTATTGGATTGGGATTACAGCAGGATTTCACAGGAAATAGATAA 419

QY 1241 GCTGTTGGGTTGTCAGCAGATGGAAGTGCATTGTGTACAGAACTGGGATTCAAATC 1300  
 DB |||||||  
 QY 420 GCTGTTGGGTTGTCAGCAGATGGAAGTGCCTTGTGTACAGAACTGGGATTCAAATC 479  
 DB |||||||  
 QY 1301 TAAAGATATGGGGTTTGGAGGACACAGCAGAGAGTGAATTTGAAGAAGATTAAACGAAAGT 1360  
 DB |||||||  
 QY 480 TAAAGATATGGGGTTTGGAGGACACAGCAGAGAGTGAATTTGAAGAAGATTAAACGAAAGT 538  
 DB |||||||  
 QY 1361 AGGAGTCAAGTCTCCAGTTGTTGGTTAAATATATCTGTAGTCGGGAAGTAAGTTTCGGTT 1420  
 DB |||||||  
 QY 539 AGGAGTCAAGTCTCCAGTTGTTGGTTAAATATATCTGTAGTCGGGAAGTAAGTTTCGGTT 598  
 DB |||||||  
 QY 1421 TGTGGAAGTGTGTTGGTTTGAATAGTGGAGTGGTTAGAAAGATTAAACTCCCTTTTGG 1480  
 DB |||||||  
 QY 599 TGTGGAAGTGTGTTGGTTTGAATAGTGGAGTGGTTAGAAAGATTAAACTCCCTTTTGG 658  
 DB |||||||  
 QY 1481 TAGTGTGCTTTGATTTATTTATTTCTTCATTTGGAACTAAACTCCCTTCAACACGCTACTC 1540  
 DB |||||||  
 QY 659 TAGTGTGCTTTGATTTATTTATTTCTTCATTTGGAACTAAACTCCCTTCAACACGCTACTC 718  
 DB |||||||  
 QY 1541 AATGTGAATTTCTGTAATCAATTTGTGTACCCAGCTTTTACTTTACTATCATCTCTTCA 1600  
 DB |||||||  
 QY 719 AATGTGAATTTCTGTAATCAATTTGTGTACCCAGCTTTTACTTTTAAAAA 778  
 DB |||||||  
 QY 1601 TATTGAACGAGAAGATAAAA 1621  
 DB |||||||  
 QY 779 AAAAAA 799  
 DB |||||||

## RESULT 6

ADH78737  
 ID ADH78737 standard; DNA; 1526 BP.  
 AC ADH78737;  
 XX  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Pea AGB1 gene ortholog, SEQ ID 17.  
 XX  
 XX Plant; agronomic trait; flowering; fruit yield; seed yield; root biomass;  
 KW seed size; seed shape; stem branch number; plant size; AGB1; gene; ds;  
 KW Pea; GPA.  
 XX  
 OS Pisum sativum.  
 XX  
 PN WO2004003146-A2.  
 XX  
 PD 08-JAN-2004.  
 XX  
 XX 24-JUN-2003; 2003WO-US020001.  
 PF  
 XX 28-JUN-2002; 2002US-0392730P.  
 PR  
 XX 05-FEB-2003; 2003US-0445208P.  
 XX  
 XX (PARA-) PARADIGM GENETICS INC.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 XX Boyes D, Davis K, Jones A, Ullah H, Chen J, Mulpuri R;  
 PI Chatterjee A, Ward MP;  
 PI  
 XX WPI; 2004-083031/08.  
 DR P-PSDB; ADH78738.  
 XX  
 XX Altering a plant agronomic trait, useful for improving plant agronomic  
 PT traits comprising regenerating plants having stably integrated expression  
 PT cassette, where the regenerated plant has an altered agronomic trait.  
 XX  
 XX Disclosure; SEQ ID NO 17; 180pp; English.  
 PS  
 XX The present invention relates to a method for altering a plant agronomic  
 CC trait selected from time to flowering, duration of flowering, fruit  
 CC yield, seed yield, root biomass, seed size, seed shape, number of stem

CC branches or size of plant. The method for altering a plant agronomic  
 CC trait comprises: introducing into a plant cell an expression cassette  
 CC comprising a nucleotide sequence operably linked to a promoter that is  
 CC operable within the plant cell, where the nucleotide sequence is selected  
 CC from: a nucleotide sequence antisense to a plant AGB1 or an AGB1 ortholog  
 CC (ADH78721-ADH78722 and ADH78725-ADH78746); a nucleotide sequence  
 CC comprising an inverted repeats of AGB1 or an AGB1 ortholog; a nucleotide  
 CC sequence encoding a dsRNA comprising a first RNA complementary to at  
 CC least 25 consecutive nucleotides of a plant AGB1 or an AGB1 ortholog and  
 CC a second RNA substantially complementary to the first RNA; a nucleotide  
 CC sequence that is AGB1 or an AGB1 ortholog; or a nucleotide sequence that  
 CC is GPAL or a GPAL ortholog (ADH78723-ADH78724 and ADH78747-ADH78781); and  
 CC regenerating a plant that has a stably integrated expression cassette  
 CC from the plant cell, where the regenerated plant has an altered agronomic  
 CC trait. The method is useful for improving plant agronomic traits  
 CC including duration of flowering, fruit yield, root biomass, seed size,  
 CC seed shape, number of stem branches or plant size. The transgenic plants  
 CC obtained are useful as parents to produce progeny plants and plant lines.

XX Sequence 1526 BP; 416 A; 268 C; 352 G; 490 T; 0 U; 0 Other;

Query Match 40.6%; Score 661.6; DB 12; Length 1526;  
 Best Local Similarity 72.8%; Pred. No. 2.2e-194;  
 Matches 882; Conservative 0; Mismatches 324; Indels 6; Gaps 2;

QY 207 AATGTCTGTCTCCGAGCTCAAAAGACGCCGCTCGCTACGGAGACGGTTAATAACCT 266  
 DB |||||||  
 QY 51 AATGTCCGTTGGGAGCTCAAAAGACGTCACATAGCAGCGACGGAACGGTTAACAATCT 110  
 DB |||||||  
 QY 267 CCGTCACACAGCTTACAGACAGACGCTCCAGCTCTCGATACCGATGTGGCAGGTTATTC 326  
 DB |||||||  
 QY 111 CAGAGAACGATTGAAGCAGACAGCGCTTCTTTGCTTGATACAGATATTCTGGATATGC 170  
 QY 327 AGCGGCGCAAGGACGCTACTCGGGTGAGCTTCGGAGCAACGGATCTGGTTGTTCGTAC 386  
 DB |||||||  
 QY 171 TAGGTCTCAAGGTAGAGCTCCTGTTACTTTTGGTCCCACTGATATTCTTTGCTAGAAC 230  
 QY 387 TCTTCAGGACACACCGGAAGGTTTATTCATTAGATTGGACCGGAGAGAACCGGAT 446  
 DB 231 GCTCAAGGTCATACCGGAAGGTTGTTATTCATTGGATTGGACTTCAGAAAAGATTAGGAT 290  
 QY 447 TCTCAGTGCATCTCAAGATGGGAGATTAACTCTGTGGGAATGCTCTAAACGAGTCAGAAAAC 506  
 DB 291 TGTGTAGTCATCCCAAGATGGGAAGATTAAATAGTGTGGAAATGCTCTTAACAGCCAGAAAAC 350  
 QY 507 TCATGCTATTAAACTCCCTTGTGCATGGGTTATGACATGTGCTTTCTCTCCAAATGGTCA 566  
 DB 351 TCATGCTATAAAGCTTCCCTTGTGCATGGGTCATGAGGTGCTTTCTCTCAACCACTGGTCA 410  
 QY 567 GTCGGTTGGTGTGGATTAGACAGTGTATGTTCTATCTTTAGCTTTAGCTTCAACGGC 626  
 DB 411 ATCTGTGTCTTGTGGGGGCTTTGACAGTGTGTTGCTCTATTTTCAATCTTTAATTTCTCCAC 470  
 QY 627 GGACAAGGATGGAACGTGTACCGGTTTCAAGATGCTCACTGCTCAGCGGGATATGTTTC 686  
 DB 471 TGATAGGGATGGGAATCTAAATGTTTTCAGGATGCTTAGTGACATAAAGGTTATGTTTC 530  
 QY 687 GTGCTGTCAAGTATGTCCCAAAATGAGGATGCCCACTTATCACCAGTTTCAGGTGATCAAAAC 746  
 DB 531 ATCTGTGATGATGTTCCAGGTGAAGACACTCACTTAATCACTGGTTCTCGAGATCAGAC 590  
 QY 747 TTGTATCTTATGGGATGTAACCTACTGTGCTCAAAACTCTCTGTTTTTGGCGGTAATTTCA 806  
 DB 591 ATGTGTTTTTATGGGATATTACTACTGGCCTTAGAACATCTGTTTTTGGAGGGGAGTTTCA 650  
 QY 807 GTCTGACATCTGCTGATGTAAGCTCTCAATCAGTGGATCAAAACCCCAAACTGGTT 866  
 DB 651 GTCTGACATCTGCTGATGTAAGCTTTAGCAATTTCCCAATTAATGATCAACTCCCAATTTGT 710  
 QY 867 TATATCTGTTTCATGCGATTCCACAGCAGGTTGTGGGACACTCTGCTGTGCAAGCCGAGC 926  
 DB 711 TGTATCTGTTCTTGGGATGCCAGCTGCCAGATTGTGGGACACTCTGCTGTGCAAGCTGAGC 770





672 ATCCGGGACACTGCGAGATGTCAAAAGTGTCTCAATAGTTTCAATCAAAACCCAGACTGTT 731  
 867 TATATCTGGTTCATGCGATTCCACAGCAGCGTTGTGGGACACTCGTGTGCGAAGCCGAGC 926  
 732 TGTATCTGGTCTCTGTGACACAACTGCTCGACTGTGGGACACCCGAGTTGCTAGTCGAGC 791  
 927 AGTGGCTACCTTTCATGGTTCACAGGAGAGATGTTAATACGGTCAAGTTCTTCCGGATGG 986  
 792 TCAACGAACATTTTATGGTTCACAGGAGAGATGTTAATACCTGTAAGTCTTCTCCCTGATGG 851  
 987 GTATAGATTGGGACTGGGATCAGACCATGGAACATCAGCCTGTATGACATAGGACTG 1046  
 852 TAATAGATTGGGACTGGGATCAGAGGATGGAACCTGCAATTAATTTGACATTAAGGACTGA 911  
 1047 TCACCAACTCCAGGT---CTATCAGGCCACATGTTGATGGTGAACCGGACCTGTGTCACTTC 1103  
 912 ACACCACTGCAAGTGTACTTACCAGCGCATGTTGATGGTGTATCCCTCATGTGACTTC 971  
 1104 CATTGCAATCTGTGTGCGGAGACTTCTTTTCGCTGGTATGCGAGCAACAACTG 1163  
 972 CATGGCAATTTCTATCTCAGCGCGTCTCTCTTTTGTGCGATATCT---AAATGGTGAITG 1028  
 1164 CTACGTTTGGGATACCTCTTGGGAGAGGTTGTTGATTTGGATTGCGGATTACAGCAGGATTC 1223  
 1029 TTATGTGTGGGACACCCCTATTAGCAAGGTGGTCTTAAACTTGGGAGGAGTTCAAAACTC 1088  
 1224 ACACAGCAATAGAAATAGCTGTTTGGGGTGTGTCAGCAGATGGAAGTGCAATTTGTACAGG 1283  
 1089 TCATGAAGGCGAATAAGTTGCTTGGGACTGTGCTGATGGAAGCGCCTTATGTACAGG 1148  
 1284 AGTTGGGATTCAAATCTAAAGATATGGCGGTTTGGAGGACACAGGAGAGTGAATTTGA 1341  
 1149 AAGTTGGGATACAAACCTGAAGATTTGGGCTTTTGGAGGGGACACAGAAGTGTGATCTGA 1206

## RESULT 8

ADH78729

ID ADH78729 standard; DNA; 1600 BP.

XX AC

XX ADH78729;

XX AC

XX 22-APR-2004 (first entry)

XX DT

XX Tobacco AGB1 gene ortholog, SEQ ID 9.

XX DE

XX plant; agronomic trait; flowering; fruit yield; seed yield; root biomass;

XX KW

XX seed size; seed shape; stem branch number; plant size; AGB1; gene; ds;

XX KW

XX Tobacco; GPA.

XX OS

XX Nicotiana tabacum.

XX XX

XX WO2004003146-A2.

XX XX

XX 08-JAN-2004.

XX XX

XX 24-JUN-2003; 2003WO-US020001.

XX XX

XX 28-JUN-2002; 2002US-0392730P.

XX PR

XX 05-FEB-2003; 2003US-0445208P.

XX PR

XX (PARA-) PARADIGM GENETICS INC.

XX PA

XX (UYNC-) UNIV NORTH CAROLINA.

XX PA

XX Boyes D, Davis K, Jones A, Ullah H, Chen J, Mulpuri R;

XX PI

XX Chatterjee A, Ward MP;

XX XX

XX WPI; 2004-083031/08.

XX DR

XX P-PSDB; ADH78730.

XX XX

XX PT

PT Altering a plant agronomic trait, useful for improving plant agronomic

PT traits comprising regenerating plants having stably integrated expression

PT cassette, where the regenerated plant has an altered agronomic trait.

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SQ

Disclosure; SEQ ID NO 9; 180pp; English.

The present invention relates to a method for altering a plant agronomic trait selected from time to flowering, duration of flowering, fruit yield, seed yield, root biomass, seed size, seed shape, number of stem branches or size of plant. The method for altering a plant agronomic trait comprises: introducing into a plant cell an expression cassette comprising a nucleotide sequence operably linked to a promoter that is operable within the plant cell, where the nucleotide sequence is selected from: a nucleotide sequence antisense to a plant AGB1 or an AGB1 ortholog (ADH78721-ADH78722 and ADH78725-ADH78746); a nucleotide sequence comprising an inverted repeats of AGB1 or an AGB1 ortholog; a nucleotide sequence encoding a dsRNA comprising a first RNA complementary to at least 25 consecutive nucleotides of a plant AGB1 or an AGB1 ortholog and a second RNA substantially complementary to the first RNA; a nucleotide sequence that is AGB1 or an AGB1 ortholog; or a nucleotide sequence that is GPAL or a GPAL ortholog (ADH78723-ADH78724 and ADH78747-ADH78781); and regenerating a plant that has a stably integrated expression cassette from the plant cell, where the regenerated plant has an altered agronomic trait. The method is useful for improving plant agronomic traits including duration of flowering, fruit yield, root biomass, seed size, seed shape, number of stem branches or plant size. The transgenic plants obtained are useful as parents to produce progeny plants and plant lines.

Sequence 1600 BP; 420 A; 343 C; 356 G; 481 T; 0 U; 0 Other;

Query Match 40.2%; Score 654.8; DB 12; Length 1600;

Best Local Similarity 74.7%; Pred. No. 3e-192;

Matches 850; Conservative 0; Mismatches 282; Indels 6; Gaps 2;

QY 207 AATGTCGTCTCGAGCTCAAGAGCGCCACGCCGTCGCTACGGAGACCGTTAATAACCT 266  
 DB 142 AATGTCAGTGCAGAGCTGAAAGAGCGGCATATGCGCCGTACACAGACTGTAAATGATCT 201  
 QY 267 CCGTGACCAAGCTTAGACAGAGACGCTCCAGCTCCGATACCGATGTCGCGAGGTATTC 326  
 DB 202 CCGTGAAGAACTTAGCAGAGAGGCTCCCAATTAATCTGACACTGATGTTCTGATATGC 261  
 QY 327 AGCGGCGCAAGGACGTTACTCGGCTGAGCTTCGGAGCAACGGATCTGGTTGTTGTCGTAC 386  
 DB 262 AAGTGCAGAGGTAAAGCTCCGCTCACCTTTGGCCCAACAGATCTGGTTGTTGTTAGGAT 321  
 QY 387 TCTTCAGGACACACCGGAAAGTTTATTCATTAGATTGACACCGGAGGAGACCGGAT 446  
 DB 322 CTTGCAAGGACACACTGGAAGGTATATTCTCTGGATTGGACTCCAGAAAGAAATCGTAT 381  
 QY 447 TGTCACTGCATCTCAAGATGGGAGATTAAATCGTGTGGAATGCTCTAACAGTCCAGAAAC 506  
 DB 382 AGTCAGTGCATCCCAAGATGGCAGATTAAATAGTGTGGAATGCTCTCACAGCCAGAAAC 441  
 QY 507 TCATGCTATTAAACTCCCTTTGTGCATGGGTATGACATGCTGCTTCTCCAAATGGTCA 566  
 DB 442 CCATGCAATTAAGCTTCCGTTGCTTGGGTATGACCTCGCCCTTCTCTAGTGGGCA 501  
 QY 567 GTCCGTTGGTGTGGTGGATTAGACAGTGTATGTTCTTATCTTTAGCCTTAGCTCAACGGC 626  
 DB 502 GTCTGTTGCTGCGGTGGCTTGGACAGTGTCTCTCTATCTTCAACTTAAATTCGCCAAT 561  
 QY 627 GGACAAAGGATGGAACCTGTACCGGTTTCAAGAAATGCTCACTGGTTCACAGGGGATATGTTTC 686  
 DB 562 CGATAAGGATGGGAACCATCTCTGTATCAAGAAATGCTTAGTGGGCATAGGGTTATGTGTC 621  
 QY 687 GTGCTGTCAAGTATGTCCTCCAAATGAGGATGCCCACTTATCACAGTTCAGGTGATCAAAC 746  
 DB 622 TTCTGTCAATATGTTCCAGATGAGGATACTCACCTTAATAACTAGTCTTGTGATCAAAC 681  
 QY 747 TTGTATCTTATGGGATGTAACCTACTCGTCTCAAAACTTCTGTTTTTGGCGGTGAATTTCA 806  
 DB 682 ATGTGCTCTTTGGGATATAAATACTACTGCTGCTTAAGAACTTCTGCTTTTGGAGGTGAGTTCA 741  
 QY 807 GTCTGACATACCTGCTGATGATCTACTAGCGCTTCAATCAGTGGATCAAAACCAACTGGTT 866

Db 742 ATCCGGGCACACTGCAGATGTACAAAGTGTCTCAATTAGTTTCATCAAAACCCAGACTGTT 801

QY 867 TATATCTGGTTTCATCGATTCACAGCAGCGTTGTGGGACACTCGTGTGCAAGCCGAGC 926

Db 802 TGTATCTGGTCTCTGTACACAACTGCTGGACTGTGGGACACCCGAGTTGCTAGTCGAGC 861

QY 927 AGTGGTACTTTCATGTCACAGGAGATGTTAATACGGTCAAGTCTTTCCGGATGG 986

Db 862 TCAACGAACATTTTATGGTTCACAGGGAGATGTTAATCTGTAAGATTTCTCCCTGATGG 921

QY 987 GTATAGATTTGGACTGAGATCAGAGATGGAACATGCGAGGCTGTATGACATAAGACTGG 1046

Db 922 TAAATAGATTTGGAATGGTTTACAGATGGAACCTGCAGATTATTTGACATTAGACTGG 981

QY 1047 TCACCAACTCCAGGT---CTATCAGCCACATGGTGATGGTGAGAACGGACCTGTCAACCTC 1103

Db 982 ACACCAAGCTGCAAGTGTACTACCAAGCGCATGGTGATGGTGATATCCCTCATGTGACTTC 1041

QY 1104 CATTCGATCTCTGTGTACGGGAGACTTTCTTTTCGGTGGCTATGGAGCAACACACTTG 1163

Db 1042 CATGGCATTTTCTATCTCAGGCCGCTTCTCTCTTTGTCGGATACTC---AAATGGTGATTG 1098

QY 1164 CTACGTTTGGGATACCTCTTCGGAGAGCTTCTATTGGATTGGGATTACAGCAGGATTC 1223

Db 1099 TTATGTGTGGGACACCCCTATTAGCAAGGTGTCCTAACTTTGGGAGGATTCAAAACCTC 1158

QY 1224 ACACAGGAATAGATAAGCTGTTTGGGGTTGTGACAGATGGAAGTGCATTTGTGTACAGG 1283

Db 1159 TCATGAAGGGCGAATAAGTTGCTGGGACTGTGAGTGAAGCGCTTATGTATACAGG 1218

QY 1284 AGTTGGGATTCAAATCTAAGATATGGCGTTTGGAGGACACAGAGAGTGAATTGA 1341

Db 1219 AAGTTGGGATACAAACCTGAAGATTTGGGCTTTTGGAGGGGACAGAAAGTGTGATCTGA 1276

RESULT 9

ID ADH78733 standard; DNA; 1434 BP.

XX AC ADH78733;

XX DT 22-APR-2004 (first entry)

XX DE Tobacco AGB1 gene ortholog, SEQ ID 13.

XX KW Plant; agronomic trait; flowering; fruit yield; seed yield; root biomass;

XX KW seed size; seed shape; stem branch number; plant size; gene; ds;

XX KW Tobacco; GPA.

XX OS Nicotiana tabacum.

XX PN WO2004003146-A2.

XX PD 08-JAN-2004.

XX PF 24-JUN-2003; 2003WO-US020001.

XX PR 28-JUN-2002; 2002US-0392730P.

XX PR 05-FEB-2003; 2003US-0445208P.

XX PA (PARA-) PARADIGM GENETICS INC.

XX PA (UNNC-) UNIV NORTH CAROLINA.

XX PI Boyes D, Davis K, Jones A, Ullah H, Chen J, Mulpuri R;

XX PI Chatterjee A, Ward MP;

XX DR WPI; 2004-083031/08.

XX DR P-PSDB; ADH78734.

XX PT Altering a plant agronomic trait, useful for improving plant agronomic

XX PT traits comprising regenerating plants having stably integrated expression

XX PT cassette, where the regenerated plant has an altered agronomic trait.

PS Disclosure; SEQ ID NO 13; 180pp; English.

XX The present invention relates to a method for altering a plant agronomic

CC trait selected from time to flowering, duration of flowering, fruit

CC yield, seed yield, root biomass, seed size, seed shape, number of stem

CC branches or size of plant. The method for altering a plant agronomic

CC trait comprises: introducing into a plant cell an expression cassette

CC comprising a nucleotide sequence operably linked to a promoter that is

CC operable within the plant cell, where the nucleotide sequence is selected

CC from: a nucleotide sequence antisense to a plant AGB1 or an AGB1 ortholog

CC (ADH78721-ADH78722 and ADH78725-ADH78746); a nucleotide sequence

CC comprising an inverted repeats of AGB1 or an AGB1 ortholog; a nucleotide

CC sequence encoding a dsRNA comprising a first RNA complementary to at

CC least 25 consecutive nucleotides of a plant AGB1 or an AGB1 ortholog and

CC a second RNA substantially complementary to the first RNA; a nucleotide

CC sequence that is AGB1 or an AGB1 ortholog; or a nucleotide sequence that

CC is GPAl or a GPAl ortholog (ADH78723-ADH78724 and ADH78747-ADH78781); and

CC regenerating a plant that has a stably integrated expression cassette

CC from the plant cell, where the regenerated plant has an altered agronomic

CC trait. The method is useful for improving plant agronomic traits

CC including duration of flowering, fruit yield, root biomass, seed size,

CC seed shape, number of stem branches or plant size. The transgenic plants

CC obtained are useful as parents to produce progeny plants and plant lines.

XX

SQ Sequence 1434 BP; 395 A; 291 C; 324 G; 424 T; 0 U; 0 Other;

Query Match 40.0%; Score 651; DB 12; Length 1434;

Best Local Similarity 74.5%; Pred. No. 4.3e-191;

Matches 848; Conservative 0; Mismatches 285; Indels 6; Gaps 2;

QY 207 AATGTCTGTCTCCGAGCTCAAAGAACGCCAGCCGTCGCTACGAGACCGTAAATAACCT 266

Db 74 AATGTCTGTCTCCGAGCTCAAAGAACGCCAGCCGTCATATGCGGCTACACAAACTGTAATATGATCT 133

QY 267 CCGTGACCCAGCTTAGACAGAGACCGCTCCAGCTCTCGATACCCAGTGTGGGAGGTATTC 326

Db 134 CCGTGAAAAACTTAAGCAGAAAGCGCTCTCCAAATTACTCGACACTGATGTATCTGGGTATGC 193

QY 327 AGCGGCGCAAGGACGTACTCCGGGTGAGCTTCGGAGCAACGGATCTGGTTTGTTCGTGTC 386

Db 194 AAGTCCGCAAGTAAACTCCGGTCATCTTTGGCCCAACAGATCTGGTTGTGTAGGAT 253

QY 387 TCTTCAGGACACACCGGAAAGGTTTATTCATATAGATTGGACACCGGAGAGAACCGGAT 446

Db 254 CTTGCAAGGACACACTGCGAAAGGTATATTCACTGGATTGGACTCCAGAAAAAGAAATCGTAT 313

QY 447 TGTCAAGTGCATCTCAAGATGGAGATTAATCGTGTGGAATGCTCTAACGAGCTCAGAAAC 506

Db 314 AGTCAGTGCATCCCAAGATGGCAGATTAAATAGTGTGGAATGCTCTCACACGCCAGAAAC 373

QY 507 TCATGCTATTAAACTCCCTTGTGCATGGGTTATGACATGTGCTTTCTCTCCAAATGGTCA 566

Db 374 CCATGCAATTAAAGCTTCCATGTGCTTGGTTATGACCTCGCGCTTCTCTCTAGTGGCA 433

QY 567 GTCGGTTCGCTGTGGTGGATTAGACAGGTATGTTTATCTTTTAGCCTTAGCTCAACCGC 626

Db 434 GTCTGTTGCCCTGCGGTGGCTTGACAGTGTCTGCTCTATCTTCAACTTAAATTCACCGAT 493

QY 627 GGACAGGATGGAACCTGTACCGGTTTCAAGAAATGCTCACTGGTCACAGGGGATATGTTTC 686

Db 494 CGATAAGGATGGGAACCATCTCTGTATCAAGAAATGCTTAGTGGGCATAGGGGTATGTGTC 553

QY 687 GTGCTGTCAAGTATGTCCCAAAATAGGATGCCCACTTATCACCAGTTTCAGGTGATCAAAAC 746

Db 554 TTCTGTCAAGTATGTTCCAGATGAGGATCTCAGCTAATAACTAGTTCTGTGTGATCAAAAC 613

QY 747 TTGTATCTTATGGGATGTAACCTACTGGTCTCAAAACTTCTGTTTGTGGCGGTGAATTTC 806

Db 614 ATGTGTCCTTTGGGATATACTACTGCGCTTAAGAACTTCTGTCTTTGGAGGTGAGTTTCA 673

QY 807 GTCTGGACATACCTCTGATGTACTAAGCTCTCAATCAGTGGATCAAAACCCAACTGGTT 866

Db 674 ATCCGGGCACACCCGACAGATGTACAAAGTGTCTCAATTAGTTTCATCAAAACCCACACTGTT 733





Db 573 TCTTCGTGTCAGTATGTTCCGGATGAGGATATCTACCTAAATAACATAGTCTCTGGTATCAA 632  
QY 745 ACTTGTATCTTATGGGATGTAATCTACTGTCTCAAAACCTTCTGTGTTTGGCGGTGAATTT 804  
Db 633 ACATGTGTAATTTGGGATATACTACTGCGCTTAAGACTTCTGTGTTTGGAGTGTGATTT 692  
QY 805 CAGTCTGGGACATGCTGATGATCTAAGCGTCTCAATCAGTGTGATCAAAACCAACCTGG 864  
Db 693 CAATCTGGGACACATGTCAGATGATCAAGTGTCTCAATAGTATCATCTAAACCCCAACTA 752  
QY 865 TTATATCTGTTCTAGTATGATTCCTCAGCAGCAGCTGTGGGACACTGTGCTCAAGCCGA 924  
Db 753 TTGTGTCCTGGGTCCTGTGACACAACTGCTGACGTGGGACACCGAGTGTCTAGTCA 812  
QY 925 GCAGTCTGCTACCTTTTCAATGTCACGAGGAGATGTTAATACGGTCAAGTCTCTTCGGAT 984  
Db 813 GCTCAACGAACATTTTCATGACACGAGAGTGTGATTTACTGTAAAGTCTTCCCTGAC 872  
QY 985 GGTATATAGATTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1044  
Db 873 GGTATATAGATTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 932  
QY 1045 GGTCAACCACTCCAGT---CTATCAGCCACATGTTGATGATGATGATGATGATGATGATGAT 1101  
Db 933 GGACACAGCTGCAAGTATATACCAACCCGATGATGATGATGATGATGATGATGATGATGAT 992  
QY 1102 TCCATTTGCAATCTCTGTGTCAGGAGACTTCTTTTCTGCTGGTGTATCGGAGCAACACT 1161  
Db 993 TCCATTTGCAATCTCTGTGTCAGGAGACTTCTTTTCTGCTGGTGTATCGGAGCAACACT 1049  
QY 1162 TGTACGTTTGGGATACCTCTTTGGGAGAGTGTGATGATGATGATGATGATGATGATGATGAT 1221  
Db 1050 TGTACGTTTGGGATACCTCTTTGGGAGAGTGTGATGATGATGATGATGATGATGATGATGAT 1109  
QY 1222 TCACACAGGATAGATAGCTGTTTGGGTTGTGACGAGATGGAAGTGCATTTGTGTACA 1281  
Db 1110 TCTCATGAAGGGGCAATAAGTGTCTGCGGACTGTCTGAGTGTGATGGAAGTGCCTTATGTACA 1169  
QY 1282 GGAAGTTGGGATTAACATCTAAAGATATGGCGCTTTTGGAGGACACAGGAGAGTGTGATGAT 1341  
Db 1170 GGAAGTTGGGATTAACATCTAAAGATATGGCGCTTTTGGAGGACACAGGAGTGTGATGATGAT 1229

RESULT 12  
ID ADH78731  
XX AC ADH78731 standard; DNA; 1560 BP.  
XX DT ADH78731;  
XX DE 22-APR-2004 (first entry)  
XX TT Tobacco AGB1 gene ortholog, SEQ ID 11.  
KW Plant; agronomic trait; flowering; fruit yield; seed yield; root biomass;  
KW seed size; seed shape; stem branch number; plant size; AGB1; gene; da;  
KW Tobacco; GPA.  
XX OS Nicotiana tabacum.  
XX PN W02004003146-A2.  
XX PD 08-JAN-2004.  
XX PF 24-JUN-2003; 2003WO-US020001.  
XX PR 28-JUN-2002; 2002US-0392730P.  
XX PR 05-FEB-2003; 2003US-0445208P.  
XX PA (PARA-) PARADIGM GENETICS INC.  
XX PA (UYNC-) UNIV NORTH CAROLINA.  
XX PI Boyes D, Davis K, Jones A, Ullah H, Chen J, Mulpuri R;

PI Chatterjee A, Ward MP;  
XX WPI; 2004-083031/08.  
DR P-PSDB; ADH78732.  
XX  
PT Altering a plant agronomic trait, useful for improving plant agronomic  
PT traits comprising regenerating plants having stably integrated expression  
PT cassette, where the regenerated plant has an altered agronomic trait.  
XX  
PS Disclosure; SEQ ID NO 11; 180pp; English.  
XX  
CC The present invention relates to a method for altering a plant agronomic  
CC trait selected from time to flowering, duration of flowering, fruit  
CC yield, seed yield, root biomass, seed size, seed shape, number of stem  
CC branches or size of plant. The method for altering a plant agronomic  
CC trait comprises: introducing into a plant cell an expression cassette  
CC comprising a nucleotide sequence operably linked to a promoter that is  
CC operable within the plant cell, where the nucleotide sequence is selected  
CC from: a nucleotide sequence antisense to a plant AGB1 or an AGB1 ortholog  
CC (ADH78721-ADH78722 and ADH78725-ADH78746); a nucleotide sequence  
CC comprising an inverted repeats of AGB1 or an AGB1 ortholog; a nucleotide  
CC sequence encoding a dsRNA comprising a first RNA complementary to at  
CC least 25 consecutive nucleotides of a plant AGB1 or an AGB1 ortholog and  
CC a second RNA substantially complementary to the first RNA; a nucleotide  
CC sequence that is AGB1 or an AGB1 ortholog; or a nucleotide sequence that  
CC is GPAL or a GPAL ortholog (ADH78723-ADH78724 and ADH78747-ADH78781); and  
CC regenerating a plant that has a stably integrated expression cassette  
CC from the plant cell, where the regenerated plant has an altered agronomic  
CC trait. The method is useful for improving plant agronomic traits  
CC including duration of flowering, fruit yield, root biomass, seed size,  
CC seed shape, number of stem branches or plant size. The transgenic plants  
CC obtained are useful as parents to produce progeny plants and plant lines.  
XX  
SQ Sequence 1560 BP; 395 A; 317 C; 338 G; 510 T; 0 U; 0 Other;  
Query Match 39.4%; Score 641.2; DB 12; Length 1560;  
Best Local Similarity 74.5%; Pred. No. 5.1e-188;  
Matches 848; Conservative 0; Mismatches 283; Indels 7; Gaps 3;  
QY 207 AATGTCTGTCTCCGAGCTCAAGAACGCGACGCCCTCGCTACGAGACCGTTAATAACCT 266  
Db 119 AATGTCTGTCTCCGAGCTCAAGAACGCGCATATGCGCGTACACAGACTGTAACTGATCT 178  
QY 267 CCGTGACACGCTTACACAGACGCGCTCCAGTCTCCGATCCGATCCGATGTCGAGGATTC 326  
Db 179 CCGTGAAACCTTAAGCAGAACGCTCTCCAAATTAATCTCGACACTGATGTTCTGGATATGC 238  
QY 327 AGCGGCGCAAGCAGCTTACTCGGCTGAGCTTCGGAGCAACGCGATCTGTTGTCGTAC 386  
Db 239 AAGTCCGCAAGTAAACTCCCGTACCTTTGGCCCAACAGATCTGTTGTTGATAGAT 298  
QY 387 TCTTCAGGACACACCGGAAAGTTTATTATTAGATTGGACACCGGAGAGAACCGGAT 446  
Db 299 CTTGCAAGGACACACTGGAAGTATATTCACTGGATTGGAATCCAGAAAAGAAATCGTAT 358  
QY 447 TGTGATGATCTCAAGATGGAGATTAATCTGTGGAATGCTCTAACAGTACAGAAAC 506  
Db 359 AGTCAGTGCATCCCAAGATGGCAGATTAATAGTGTGAATGCTCTCACAAAGCCAGAAAC 418  
QY 507 TCATGCTATTAAACTCCCTTGTGATGGGTATGACATGCTGTTTCTCTCCAAATGGTCA 566  
Db 419 CCATGCAATTAAGCTTCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478  
QY 567 GTCGGTTGGCTGTGGGATTAGACAGTGTATGTTCTATCTTTAGCCTTAGCTCAACCGC 626  
Db 479 GTCTGTTGCTGCGGTGGCTTTGACAGTGTCTGCTCTATCTAACTTAAATTCGCAAT 538  
QY 627 GGACAAAGGATGGAACCTGTACCGGTTTCAAGATGCTCACTGTGTCACAGGGGATATGTTTC 686  
Db 539 CGATAAGGATGGGAACCATCTCTGTATCAAGAAATGCTTAGTGGGCATTAAGGTTATGTGTC 598  
QY 687 GTGCTGTAGTATGTCCTCCAAATGAGGATGCCCACTTATCACCAGTTCAGGTGATCAAAAC 746

Db 599 TTCCTGTCAATATGTTCCAGATGAGATACTCACCTAATAACTAGTCTTGGTGATCAAAC 658  
Qy 747 TTGTATCTTATGGGATGAACACTCTCTCAAAACTTCTGTCTTTTGGCGGTGAATTTCA 806  
Db 659 ATGTGTCTCTTGGGATATAACTACTAGTCTTCTAGAACTTCTGTCTTTGGAGGTGAGTTCA 718  
Qy 807 GTCCTGACATATCTGTGATGATCACTAAGCGTCTCAATAGTGGATCAAAACCCAACTGGTT 866  
Db 719 ATCCGGGCACACTGCAGATGTACAAAGTGTCTCAATATTAGTTTCATCAAAACCCAGACTGTT 778  
Qy 867 TATATCTGTCTCATCGATTTCCACAGCAGGTGTGGGACACTCTGTCTGCAAGCCGAGC 926  
Db 779 TGTATCTGGTCTCTGTGACAACTGTCTCGACTGTGGGACAAACCGAGTTGCTAGTCGAGC 838  
Qy 927 AGTGGTACCTTTTCATGTTCCAGAGGAGATGTTAATACGGTCAAGTCTTTTCCGGATGG 986  
Db 839 TCAACGAACATTTTATGGTTCACGAGGAGATGTTAATACTGTAAAGTCTTCCCTGATGG 898  
Qy 987 GTATAGATTTGGGACTGGATCAGACGATGGAAACATGCGAGGCTGTATGACATAAGACTGG 1046  
Db 899 TAAATAGATTTGGAACCTGTTTCAGAGGATGGAACCTGCAGATTAATTTGACATTTAGACTGG 958  
Qy 1047 TCACCAACTCCAGGT---CTATCAGCCACATGCTGATGTGTGAGAACGGACCTGTCACTTC 1103  
Db 959 ACACGAGCTGCAGTGTACTACACCGCATGTGTGATGTGATATCCCTCATGTGACTTC 1018  
Qy 1104 CATTGCATTTCTGTGTGAGGAGACTTCTTTTCGCTGGCTATGCGAGCAACAACTTG 1163  
Db 1019 CATGCAATTTCTATCTCAGGCGCTTCTCTTTGTCGGATATC--AAATGTGTATG 1075  
Qy 1164 CTACGTTTGGGATACCTCTTGGGAGAGTGTGTATTTGGATTTGGGATTTACAGCAGATTC 1223  
Db 1076 TTATGTGTGGGACACCTTATTAGCAAAAGGTGTCTTAAACTTTGGGAGGATTTCAAAACTC 1135  
Qy 1224 ACACAGGAATAGAATAAGCTGTTTCGGGTGTGTGACAGATGGAAGTGCATTTGTGTACAGG 1283  
Db 1136 TCATGAAGGGCGAATAAGTTGCTGGACTGTGAGTGTGATGGAAGCGCTTATGTACAGG 1195  
Qy 1284 AAGTTGGGATTCAAATCTAAAGATATGGCGCTTTGGAGGACACAGGAGAGTGATTTGA 1341  
Db 1196 AAGTTGGGATCAAAACCTGAAGATTTGGGCTTTTGGAGG-GACAGAGTGTGATCTGA 1252

## RESULT 13

ADH78727  
ID ADH78727 standard; DNA; 1524 BP.  
XX AC ADH78727;  
XX DT 22-APR-2004 (first entry)  
XX DE Potato AGB1 gene ortholog, SEQ ID 7.  
KW Plant; agronomic trait; flowering; fruit yield; seed yield; root biomass;  
KW seed size; seed shape; stem branch number; plant size; AGB1; gene; ds;  
KW Potato; GPA.  
XX OS Solanum tuberosum.  
XX PN WO2004003146-A2.  
XX PD 08-JAN-2004.  
XX PF 24-JUN-2003; 2003WO-US020001.  
XX PR 28-JUN-2002; 2002US-0392730P.  
XX PR 05-FEB-2003; 2003US-0445208P.  
XX PA (PARA-) PARADIGM GENETICS INC.  
XX PA (UYN-) UNIV NORTH CAROLINA.  
XX PI Boyes D, Davis K, Jones A, Ullah H, Chen J, Mulpuri R;  
PI Chatterjee A, Ward MP;

XX

WPI; 2004-083031/08.  
P-PSDB; ADH78728.

Altering a plant agronomic trait, useful for improving plant agronomic traits comprising regenerating plants having stably integrated expression cassette, where the regenerated plant has an altered agronomic trait.

Disclosure; SEQ ID NO 7; 180pp; English.

The present invention relates to a method for altering a plant agronomic trait selected from time to flowering, duration of flowering, fruit yield, seed yield, root biomass, seed size, seed shape, number of stem branches or size of plant. The method for altering a plant agronomic trait comprises: introducing into a plant cell an expression cassette comprising a nucleotide sequence operably linked to a promoter that is operable within the plant cell, where the nucleotide sequence is selected from: a nucleotide sequence antisense to a plant AGB1 or an AGB1 ortholog (ADH78721-ADH78722 and ADH78725-ADH78746); a nucleotide sequence comprising an inverted repeats of AGB1 or an AGB1 ortholog; a nucleotide sequence encoding a dsRNA comprising a first RNA complementary to at least 25 consecutive nucleotides of a plant AGB1 or an AGB1 ortholog and a second RNA substantially complementary to the first RNA; a nucleotide sequence that is AGB1 or an AGB1 ortholog; or a nucleotide sequence that is GPA1 or a GPA1 ortholog (ADH78723-ADH78724 and ADH78747-ADH78781); and regenerating a plant that has a stably integrated expression cassette from the plant cell, where the regenerated plant has an altered agronomic trait. The method is useful for improving plant agronomic traits including duration of flowering, fruit yield, root biomass, seed size, seed shape, number of stem branches or plant size. The transgenic plants obtained are useful as parents to produce progeny plants and plant lines.

Sequence 1524 BP; 434 A; 303 C; 334 G; 453 T; 0 U; 0 Other;

Query Match 39.3%; Score 640.8; DB 12; Length 1524;

Best Local Similarity 73.9%; Pred. No. 6.7e-188;

Matches 842; Conservative 0; Mismatches 292; Indels 6; Gaps 2;

Qy 205 GGAATGTCTGTCTCCGAGCTCAAAAGAACGCCACCGCTCGCTACGGAGACCGTTAATAAC 264

Db 46 GAATGTCTGTCTCCGAGCTCAAAAGAACGCCACCGCTCGCTACGGAGACCGTTAATAAC 105

Qy 265 CTCCTGTACAGCTTAGACAGAGACGGCTCCAGCTCTCTCGATACCGATGTGGCGAGTAT 324

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Qy 325 TCAGCGCGCAAGGACGTACTCGGGTGAGCTTCGGAGCAAGGATCTGTTTGTGTCGT 384

Db 166 GCAAGAGGCAAGGTAAAGTCCGGTAACTGTCGGCCCAACAGATCTAGTTTGTGAGG 225

Qy 385 ACTCTTCAGGGACACACCGGAAAGTTTATTATTAGATTGGACACCGGAGGAACCGG 444

Db 226 ATCTGTCAAGACACACATGGAAAGTCTATTCACTGGACTGGATCTCTGGAATAATCGT 285

Qy 445 ATTGTCTAGTGCATCTCAAGATGGGAGATTAATCTGTGGAATGCTCTAAACGAGTCAGAAA 504

Db 286 ATAGTCTAGTGCATCCCAAGATGTAGATTAAATAGTGTGGAATGCTCTCAACAGCCAGAAA 345

Qy 505 ACTCATGCTATTAACTCCCTTGTGCATGGTTATGACATGTGCTTCTCTCCAATGGT 564

Db 346 ACCCATGCAATTAAAGCTTCCATGTGCTTGGGTATAGACCTGTGCTTCTCTCTAGTGG 405

Qy 565 CAGTCTGGTGTGGTGGATTAGACAGATGTATGTTCTATCTTTAGCTTAGCTTCAACG 624

Db 406 CAGTCTGTGTGTGTGGCGGCTTGAACAGTGCCTGCTCTATCTTCAACTTAATTTACCA 465

Qy 625 CGGACCAAGGATGGAATGTACACCGTTTCAAGAAATGCTCACTGTGTACAGGGATATGTT 684

Db 466 ATCGATAAGGATGGGATCCATCCAGTATCGAAGATGCTTAGTGGGCATTAAGGGGTATGTG 525

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Db 526 TCTTCGTGTAGTATGTTCCGGATGAGGACTACTCACCTAATAACTAGTCTCTGGGTATCA 585







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PR	20-JUL-1999;	99US-0144348P.	PR	14-OCT-1999;	99US-0159343P.	586	TTAGACAGTGTATGTTTCTATTCTTTAGACCTTACCTCAACGGCGGACCAAGGATGGAACTGTA	645					
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Search completed: December 28, 2005, 15:33:31  
Job time : 949 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2005, 13:54:02 ; Search time 5978 Seconds  
(without alignments)  
12749.441 Million cell updates/sec

Title: US-10-602-898A-1  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: EST:\*

1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_hic: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_est7: \*  
9: gb\_gss1: \*  
10: gb\_gss2: \*  
11: gb\_gss3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	748.6	46.0	896	2	BE037621
5	565	34.7	663	1	AV823429
6	554.4	34.0	590	1	AV784390
7	552.2	33.9	1685	4	AY109568
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9	522	32.0	978	7	CK248467
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12	513.2	31.5	535	1	A1994586
13	511.4	31.4	838	7	CO072562
14	506.6	31.1	645	1	AM058772
15	504.6	31.0	778	8	DN620362
16	504.2	31.0	829	7	CO125466
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19	477.2	29.3	783	8	CK050448
20	476.8	29.3	804	2	BG647926
21	470.2	28.9	879	6	CF203907
22	466.4	28.6	783	3	BI422788

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25	459	28.2	885	8	DR912730	DR912730	EST110426
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27	449	27.6	461	6	CD528998	CD528998	01E12 Ara
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29	442.4	27.2	714	6	CD835721	CD835721	BN45.046H
30	437.6	26.9	713	8	DN958590	DN958590	USDA-FP/A
31	435.4	26.7	663	7	CNS19259	CNS19259	QQ0104 B3
32	435.4	26.7	870	8	DR925535	DR925535	EST11707
33	431	26.5	810	2	BG646074	BG646074	EST507693
34	429.2	26.3	817	5	BG583121	BG583121	EST484871
35	425.6	26.1	686	5	BQ860248	BQ860248	QCC15D22.
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45	406.8	25.0	421	3	BP606162	BP606162	BP606162

## ALIGNMENTS

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DEFINITION  
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone  
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(thale cress).  
ACCESSION  
BX828861  
VERSION  
BX828861.1 GI:42461179  
KEYWORDS  
HTC; GSIT cDNA.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
REFERENCE  
1 (bases 1 to 1537)  
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,  
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,  
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.  
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:  
A Combined Approach to Evaluate and Improve Arabidopsis Genome  
Annotation  
Unpublished  
2 (bases 1 to 1537)  
Genoscope.  
Direct Submission  
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr)  
The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out  
full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli  
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,  
Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis  
Genome released by MIPS (Munich Information center for Protein  
Sequences) . 5 prime and 3 prime are assembled with Phrap.  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full  
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DB	23	CGTGTTCGTCCTGACATGATCTCTCTCAAGCTTTTAAATCTCTCTCTTTTCCCA	82						
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QY	253	ACCGTTAATACCTCCGTGACCATCTTAGACAGACGCGCTCCAGCTCTCGATACCGAT	312						
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QY	313	GTGCGGAGGATTTACGCGCGCAAGAGCTACTCGGGTGAGCTTCGGAGCAACGATCTG	372						
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DB	383	GTTCGTTCGCTACTCTTCAGGACACACCGGAAAGTTTATTCATTAAGATTGGACACCG	442						
QY	433	GAGAGAACCGGATTTGTCAGTGCATCTCAAGATGGAGATTAATCGTGGAACTGCTTA	492						
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QY	493	ACGAGTCAGAAACTCATGCTATTAACCTCCCTTGTCATGGGTTATGACATGCTCTTC	552						
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QY	613	CTTAGCTCAACGGCGGACAAAGATGGAATGACCGGTTTCAAGATGCTACTGCTGAC	672						
DB	623	CTTAGCTCAACGGCGGACAAAGATGGAATGACCGGTTTCAAGATGCTACTGCTGAC	682						
QY	673	AGGGGATATGTTTCGTGCTGTCAAGTATGCCAAATGAGGATGCCACCTATACCAAGT	732						
DB	683	AGGGGATATGTTTCGTGCTGTCAAGTATGCCAAATGAGGATGCCACCTATACCAAGT	742						
QY	733	TCAGTGTATCAAACTTGATCTTATGGGATGTAATCTAGTGTCTCAAACTCTCTGTTTT	792						
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QY	853	AACCCAAACTGGTTTATATCTGGTTCATGCGATTCACAGCACGGTTGTGGACACTCGT	912						
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DEFINITION	Arabidopsis thaliana (thale cress).					
ACCESSION	BX828483					
VERSION	BX828483.1 GI:42461795					
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SOURCE	Arabidopsis thaliana (thale cress)					
ORGANISM	Arabidopsis thaliana					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.					
AUTHORS	Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.					
TITLE	Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 1527)					
AUTHORS	Genoscope.					
TITLE	Direct Submission					
JOURNAL	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)					

**COMMENT**

The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. [http://www.genoscope.cns.fr/externe/sequences/Banque\\_Projet\\_EF/Full\\_length](http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length)  
<http://www.genoscope.cns.fr/cgi-bin/qab/qab?source=Arabidopsis>.

## FEATURES

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## ORIGIN

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1765)  
Castelli, V., Aury, J.M., Jallion, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, P., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.

Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

Unpublished  
2 (bases 1 to 1765)  
Genoscope.

Direct Submission  
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full length  
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Matches 1512; Conservative 0; Mismatches 1; Indels 240; Gaps 2;

QY 22 GTCCTGACTGATCTCTCAAGCTTTTAAATCTCTCTCTTTCCACGTAATTC 81  
DB 1 GCTTGACTGATCTCTCTCAAGCTTTTAAATCTCTCTCTTTCCACGTAATTC 60  
QY 82 CCCAAATCCATCTTTCTAGGGTTCGATCTCCCTCTCTCAATCATGAACCTTCTCTCT 141  
DB 61 CCCAAATCCATCTTTCTAGGGTTCGATCTCCCTCTCTCAATCATGAACCTTCTCTCT 120  
QY 142 CTAGACCCCAAAAGTTTCCCTTTTATTTGATCGGCGACGGAGAACCTTAAGTCTGAT 201  
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QY 202 CCCGGAATGTCGTCTCCGAGCTCAAGAAGCCACGCCGCTCGCTACCGAGACCGTTAAT 261  
DB 181 CCCGGAATGTCGTCTCCGAGCTCAAGAAGCCACGCCGCTCGCTACCGAGACCGTTAAT 240  
QY 262 AACCTCCGTGACCGAGCTTAGACAGAGCGCTTCCAGCTCTCCGATACCGATGTGCGGAGG 321  
DB 241 AACCTCCGTGACCGAGCTTAGACAGAGCGCTTCCAGCTCTCCGATACCGATGTGCGGAGG 300  
QY 322 TATTACGGCGGCGAAGGACGTACTCGGGTGAGCTTCGGAGCAACGGATCTGGTTTGTGT 381  
DB 301 TATTACGGCGGCGAAGGACGTACTCGGGTGAGCTTCGGAGCAACGGATCTGGTTTGTGT 360  
QY 382 CGTACTCTTCAGGGACACACCGGAA----- 406

DB Db 361 CGTACTCTTCAGGACACACCGGAAAGGTGACTCAAAAGTTTGGCATCTTTATCTCTTCAAGC 420  
QY 407 ----- 406  
DB Db 421 ATGCTTCTTTGGAGTGTTTCTAGCCTGTGATATAAAAGCTTCCATTTTGGGGTTGTAT 480  
QY 407 ----- 406  
DB Db 481 CTAGTTGTTTATTTAGTTGGTGTGTTTATAAGATGTTACCAGTTATCATGTATGAGGAT 540  
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QY 407 -----AGTTTATTTCATTAGATTGGACACCGGAGAGAAC 442  
DB 601 GTTGATTTAACATGTGGGATTTGACAGTTTATTCATTAGATTGGACACCGGAGAGAAC 660  
QY 443 GGATTGTCAGTGATCTCAAGATGGGAGATTAATCGTGTGGAATGCTCTAACGAGTCAGA 502  
DB 661 GGATTGTCAGTGATCTCAAGATGGGAGATTAATCGTGTGGAATGCTCTAACGAGTCAGA 720  
QY 503 AAACCTCATGCTATTAACTCCCTTGTGCATGGGTTATGACATGCTTCTCTCCAAATG 562  
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QY 563 GTCAGTCGGTTGCGTGTGGATTTAGACAGTGATGTTCTTATCTTTAGCCCTTAGCTCAA 622  
DB 781 GTCAGTCGGTTGCGTGTGGATTTAGACAGTGATGTTCTTATCTTTAGCCCTTAGCTCAA 840  
QY 623 CGGCGGACAGGATGGAACTGTACCGGTTTCAAGAAATGCTCACTGGTTCACAGGGGATG 682  
DB 841 CGGCGGACAGGATGGAACTGTACCGGTTTCAAGAAATGCTCACTGGTTCACAGGGGATG 900  
QY 683 TTTTCGTCTGTCACTATGTCCTCAATGAGGATGCCACCTTATCACCAGTTTCAAGTTGATC 742  
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QY 923 GAGCAGTCGTAACCTTTTCATGGTTCAGGAGGAGATGTTAATACGGTCAAGTTTCTTTCGG 982  
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DB 1321 CCATTGCAATCTCTGTGTGTCAGGGAGACTTCTTTTCGCTGGCTATGCGAGCAACACACTT 1380  
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DB 1381 GCTACGTTTGGGATACCCCTCTTGGGAGAGGTTGTTATTTGGATTTGGGATTTACAGCAGATT 1440  
QY 1223 CACACAGGAATAGAAATAAGCTGTTTGGGTTGTTCAGCAGATGGAAGTGCAATGTTGTACAG 1282  
DB 1441 CACACAGGAATAGAAATAAGCTGTTTGGGTTGTTCAGCAGATGGAAGTGCAATGTTGTACAG 1500



Qy	1283	GAAGTTGGGATTCAAATCTTAAAGATATGGCGTTTGGAGGACACAGAGAGTGAATTTGAA	1342					
Db	1501	GAAGTTGGGATTCAAATCTTAAAGATATGGCGTTTGGAGGACACAGAGAGTGAATTTGAA	1560					
Qy	1343	GAAGATTTAAACGAAAGCTAGGAGTCAAGTCTCCAGTTTGGTTTAAATATATCTGTAGTC	1402					
Db	1561	GAAGATTTAAACG-NAAGTAGAGTCAAGTCTCCAGTTTGGTTTAAATATATCTGTAGTC	1619					
Qy	1403	GGGAAGTAAGGTTCCGTTTGTGGAAAGTGTGTGGTTTGGAAATAGTGAGTGGTTAGAAGA	1462					
Db	1620	GGGAAGTAAGGTTCCGTTTGTGGAAAGTGTGTGGTTTGGAAATAGTGAGTGGTTAGAAGA	1679					
Qy	1463	ATTTAAACTTCCCTTTTGTAGTGTCTTGAATTTATTTATTTCTCATTTGGGAACCTAAAC	1522					
Db	1680	ATTTAAACTTCCCTTTTGTAGTGTCTTGAATTTATTTATTTCTCATTTGGGAACCTAAAC	1739					
Qy	1523	TCCCTTCAACACGC	1535					
Db	1740	TCCCTTCAACACGC	1752					
RESULT 4								
BE037621								
LOCUS								
DEFINITION	BE037621	896 bp mRNA linear	EST 07-JUN-2000					
AA01H1 AA Arabidopsis thaliana cDNA 5' similar to guanine								
nucleotide-binding protein beta subunit, mRNA sequence.								
ACCESSION	BE037621							
VERSION	1	GI:8332637						
KEYWORDS	EST.							
SOURCE	Arabidopsis thaliana (thale cress)							
ORGANISM	Arabidopsis thaliana							
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;								
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.								
REFERENCE	1 (bases 1 to 896)							
AUTHORS	Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C., Scarra, G., Wheeler, M. and Zepeda, G.R. Functional Genomics of Plant Stress Tolerance Unpublished (2000) Contact: Michalowski, C.B. University of Arizona Bio Sciences West room 513, Tucson, AZ 85721, USA Tel: 520-621-7982 Fax: 520-621-1697 Email: cbm@u.arizona.edu An open reading frame exists. Location/Qualifiers							
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/organism="Arabidopsis thaliana"								
/mol_type="mRNA"								
/ecotype="Columbia"								
/db_xref="taxon:3702"								
/tissue type="leaves, flowering plants"								
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/clone.lib="A8"								
/note="20 h 200mM NaCl"								
ORIGIN								
Query Match	46.0%;	Score 748.6; DB 2; Length 896;						
Best Local Similarity	95.1%;	Pred. No. 7.5e-210;						
Matches	826; Conservative	0; Mismatches 36; Indels 7; Gaps 5;						
Qy	35	CTTCTCAAGCTTTTAAATCTCTCTCTTTCCGACGTAATTCGCCCAATCCATTC	94					
Db	28	CTTCTCAAGCTTTTAAATCTCTCTCTTTCCGACGTAATTCGCCCAATCCATTC	87					
Qy	95	TTTCTAGGGTTCGATCTCCCTCTCTCAATCATGAACCTTCTTCTTCTAGACCCCAAA	154					
Db	88	TTTCTAGGGTTCGATCTCCCTCTCTCAATCATGAACCTTCTTCTTCTAGACCCCAAA	147					
Qy	155	AGTTTCCCCCTTTTATTTTGAATCGGCGACGGAGAAGCCCTAAAGTCTGATCCCGGAATGTCTG	214					

Plant Functional Genomics Research Group RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-4359 Fax: 81-298-36-9060 Email: meeki@rtc.riken.go.jp An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site ( <a href="http://www.gsc.riken.go.jp/e/plant/index_e.html">http://www.gsc.riken.go.jp/e/plant/index_e.html</a> ) for further details.	
FEATURES	Location/Qualifiers
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	/clone="RAPL05-19-B08"
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	/lab_host="SOLR"
	/clone_lib="RAPLS"
	/note="Site 1: SstI; Site 2: XhoI; subjected to dehydration-treated(1,2,5,10,24 hr)"
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Query Match 34.7%; Score 565; DB 1; Length 663; Best Local Similarity 98.2%; Pred. No. 1.8e-155; Matches 601; Conservative 0; Mismatches 8; Indels 3; Gaps 3;	
Qy	13 CGTGTGTGTGCTTGACGTATCTCTCTCAAGCTTTTTTAAATCTCTCTCTTTTCCCA 72
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Qy	73 CGTAATTCCTCCCAATCCATCTTTCTAGGTTGATCTCCCTCTCTCAATCATGAACCT 132
Db	106 CGTAATTCCTCCCAATCCATCTTTCTAGGTTGATCTCCCTCTCTCAATCATGAACCT 165
Qy	133 TCCTCTCTCTAGACCCACAAAGTTTCCCTTTTATTTGATCGGCGACGAGAGCCT 192
Db	166 TCCTCTCTCTAGACCCACAAAGTTTCCCTTTTATTTGATCGGCGACGAGAGCCT 225
Qy	193 AAGTCTGATCCCGAATGCTGTCTCCGAGTCAAGAACGCCGCGTCCGTACGGAG 252
Db	226 AAGTCTGATCCCGAATGCTGTCTCCGAGTCAAGAACGCCGCGTCCGTACGGAG 285
Qy	253 ACCGTTAATAACCTCCGTGACAGCTTAGACAGACGCCCTCCAGCTCTCTCGATA -CGGA 311
Db	286 ACCGTTAATAACCTCCGTGACAGCTTAGACAGACGCCCTCCAGCTCTCTCGATACCGGA 345
Qy	312 TGTGGCGAGGATTCAGCGGCGCAAGGACGTACTCGGTGAGCTTCGGAGCAACGGATCT 371
Db	346 TGTGGCGAGGATTCAGCGGCGCAAGGACGTACTCGGTGAGCTTCGGAGCAACGGATCT 405
Qy	372 -GGTTTGTGTGCTACTCTTCAGGAGACACCGGAAA -GGTTTATTATTAGATTGGACA 429
Db	406 GGGTGTGTGTGCTACTCTTCAGGAGACACCGGAAAGGGTTTATTATTAGATTGGACA 465
Qy	430 CCGGAGAGGAACCGGATGTTCAGTGCATCTCAAGATGGGAGATTAATCGTGTGGAATGCT 489
Db	466 CCGGAGAGGAACCGGATGTTCAGTGCATCTCAAGATGGGAGATTAATCGTGTGGAATGCT 525
Qy	490 CTAACGAGTCAGAAACATCTGCTATTAACTCCCTTGTGATGGGTTATGACATGTGCT 549
Db	526 CTAACGAGTCAGAAACATCTGCTATTAACTCCCTTGTGATGGGTTATGACATGTGCT 585
Qy	550 TTCTCTCCAAATGGTCAGTGGTGGTGGTGGATAGACAGTGTATGTTCTATCTTT 609
Db	586 TTCTCTCCAAATGGTCAGTGGTGGTGGTGGATAGACAGTGTATGTTCTATCTTT 645
Qy	610 AGCCTTAGCTCA 621
Db	646 AGCCTTAGCTAA 657
RESULT 6 AV784390/c LOCUS DEFINITION AV784390 RAPL5 Arabidopsis thaliana cDNA clone RAPL05-19-B08 3', mRNA sequence. ACCESSION AV784390 VERSION AV784390.1 GI:19803180 KEYWORDS EST. SOURCE Arabidopsis thaliana (thale cress) ORGANISM Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses. REFERENCE 1 (bases 1 to 590) AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Ono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K. TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b) JOURNAL Unpublished (2002) COMMENT Contact: Motoaki Seki Plant Functional Genomics Research Group RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-4359 Fax: 81-298-36-9060 Email: meeki@rtc.riken.go.jp An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site ( <a href="http://www.gsc.riken.go.jp/e/plant/index_e.html">http://www.gsc.riken.go.jp/e/plant/index_e.html</a> ) for further details.	
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Qy	983 ATGGGTATAGATTGGGACTGGATCAGACGATGGAAATCGAGCTGTATGACATAAGGA 1042
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Qy	1043 CTGGTCCCAACTCCAGGTCTATCAGCCACATGTGTGATGGTGGAGACGGACCTGCACCT 1102
Db	530 CTGGTCCCAACTCCAGGTCTATCAGCCACATGTGTGATGGTGGAGACGGACCTGCACCT 471
Qy	1103 CCATTGCATTCTCTGTCTCAGGGAGACTCTTTTCGCTGGCTATGCCAGCAACAACACTT 1162
Db	470 CCATTGCATTCTCTGTCTCAGGGAGACTCTTTTCGCTGGCTATGCCAGCAACAACACTT 411
Qy	1163 GCTACGTTTGGGATACCCCTCTTGGGAGAGGTTGTATTGGATTTGGGATTTACAGCAGGATT 1222
Db	410 GCTACGTTTGGGATACCCCTCTTGGGAGAGGTTGTATTGGATTTGGGATTTACAGCAGGATT 351
Qy	1223 CACACAGGATAGATTAAGCTGTTTGGGTTGTTCAGCAGATGGAACTGTCATTGTGTACAG 1282
Db	350 CACACAGGATAGATTAAGCTGTTTGGGTTGTTCAGCAGATGGAACTGTCATTGTGTACAG 291
Qy	1283 GAAGTTGGGATTCAAATCTAAAGATATGGGGTTTGGAGGACACAGAGAGTGAATTTGAA 1342
Db	290 GAAGTTGGGATTCAAATCTAAAGATATGGGGTTTGGAGGAC -CAGGAGAGTGAATTTGAA 232

QY 1343 GAAGATTTAAAGAAAGTAGGAGTCACGCTCCAGTCTTGGTTAAATATATCTGTAGTC 1402  
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Db 231 GAAGATTTAAAGC-AAAGTAGGAGTCACGCTCCAGTCTTGGTTAAATATATCTGTAGTC 173  
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QY 1403 GGAAGTAGTAAAGTTCCGTTTGGTGAAGTGTGGTTTCAAAATAGTGGAGTGTAGAAGA 1462  
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Db 172 GGAAGTAGTAAAGTTCCGTTTGGTGAAGTGTGGTTTCAAAATAGTGGAGTGTAGAAGA 113  
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QY 1463 ATTAACCTCCCTTTTGTGA-GTGTGCTTGAATTTATTTATTTCTTCATTTGGAACTAAA 1521  
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Db 112 ATTAACCTCCCTTTTGTAGTGTGCTTTGATTTATTTATTTCTTCATTTGGAACTAAA 53  
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QY 1522 CTCCTTCAACGCTACTCAATGTAATCTGTAAATCAATTTGTGTACCACC 1573  
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RESULT 7  
AY109568  
LOCUS Zea mays CL2390\_1 mRNA linear HTC 25-FEB-2005  
DEFINITION Zea mays 1685 bp mRNA sequence.  
ACCESSION AY109568  
VERSION AY109568.1 GI:21213336  
KEYWORDS HTC.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE  
AUTHORS Gardiner, J., Schroeder, S., Polacco, M.L., Sanchez-Villeda, H., Fang, Z., Morgante, M., Landewe, T., Flegler, K., Useche, F., Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H. Jr.  
TITLE Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization  
JOURNAL Plant Physiol. 134 (4), 1317-1326 (2004)  
PUBMED 15020742  
REFERENCE 2 (bases 1 to 1685)  
AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.  
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes  
JOURNAL Unpublished (2002)  
REFERENCE 3 (bases 1 to 1685)  
AUTHORS Coe, E.H.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

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Location/Qualifiers  
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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 33 9%; Score 552.2; DB 4; Length 1685;  
Best Local Similarity 66.8%; Pred. No. 1.5e-151;  
Matches 805; Conservative 0; Mismatches 388; Indels 12; Gaps 2;

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QY 255 CGTTAATAACCTCCGTGACAGCTTAGACAGAGAGCGCTCCAGCTCCTCGATACCGATGT 314  
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Db 246 GGTGAACCTCCCTGCGGAGCGCTCCGCCAGCGCGGAGAGCGTCTCTCGACACCGAGCT 305  
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QY 375 TTGTTGTCGTACTCTTCAGGGACACACCGGAAAGGTTTATTTATTTAGATTTGGACACCG 434  
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QY 435 GAGGAACCGGATTTGTCAGTGCATCTCAAGATGGGAGATTAATCGTGTGGAATGCTCTAAC 494  
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Db 426 AAAGAAATTGGATAGTCACTGCTCTCAAGATGGAAGGTTAATTTGTGGAAATGCAATTGAC 485  
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Db 486 AAGCCAGAAAACACATGCTCAAAAGCTGCAATGCCATGGGTTATGGGTTGCTTTTTCG 545  
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QY 1206 GGGATTACAGCAGGATTTCACAGGAAATAGATNAGCTGTTTGGGGTTTGTCTCAGCATGG 1265  
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205 GGAATGTCGTCTCCGAGCTCAAGAAAGCCGACGCGGTGCTACGGAGACCGTTAAATAC 264  
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 81 GAAATGTCTAGTTCGGAGCTGAAGAGCGGCACATGGCCGCTACACAGACTGTAAATGAT 140  
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 265 CTCCTGTGACGCTTAGACAGAGAGCGCTCCAGCTCCCTCGATACCGATGTGCGGAGGTAT 324  
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 141 CTCCTGTGAAAACTTAAGCAGAGAGCGTCTCCAACTTACTCGACAGAGATTTCTGGGTAT 200  
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 685 TCGTGTGTCAGTATGTCCCAATAGGAGTGCACCTTATATCAACGATTCAGGTGATCAA 744  
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 621 ACATGTGTACTTTGGGATATACTACTGGCTTAAGAACTTCTGTGTTGGAGGTGAGTTT 680  
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 865 TTTATATCTGGTTTCATGCGATTCACAGACGCTTGTGGGACACTGCTGTCGAAGCCGA 924  
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 741 TTTGTGCTGGTCTGTGACAACTGCTCGACTGTGGGACACCGAGTTGCTAGTGA 800  
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 925 GCAATGCGTACCTTTTCATGTCACGAGGAGATGTTAATACGGTCAAGTTCTTTCGGAT 984  
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 801 GCTCAACGAACATTTCAATGACACGAGAGTGTATCTACTGTAAAGTTCTTCCCTGAC 860  
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 985 GGTATAGATTTGGGACTGGATCAGACGATGGAACATGCAAGCTGTATGACATAAGGACT 1044  
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 861 GGTATAGATTTGGGACTGGTTCAGATGATGGAGCTGAGATTTTACATTTAGACT 920  
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 921 GGACACCACTGCAAGTATACAAACCAACCGCATGGTGGAGTGCATCCCTCATGTGA 978  
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RESULT 10  
 LOCUS CO122720  
 DEFINITION GR\_Eb04H21.f GR\_Eb Gossypium raimondii cDNA clone GR\_Eb04H21 5', mRNA sequence.  
 ACCESSION CO122720  
 VERSION CO122720.1 GI:48821407  
 KEYWORDS EST.  
 SOURCE Gossypium raimondii  
 ORGANISM Gossypium raimondii  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosoids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 858)  
 Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,  
 Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and  
 Wing,R.A.  
 Global assembly of Cotton ESTs  
 Unpublished (2004)  
 Contact: Rod A. Wing  
 Arizona Genomics Institute  
 The University of Arizona  
 Forbes Building Room 303, Tucson, AZ, 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: rwing@genome.arizona.edu  
 Plate: 04 row: H column: 21.  
 Location/Qualifiers  
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 1. 858  
 /organism="Gossypium raimondii"  
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 /db\_xref="taxon:29730"  
 /clone="GR\_Eb04H21"  
 /tissue\_type="floral"  
 /dev\_stages="3 to +3 DPA"  
 /lab\_host="DH10B"  
 /clone\_lib="GR\_Eb"  
 /note="Vector: PCMV.SPORT-6.1; Site 1: NotI; Site 2:  
 EcoRV; library made by invitrogen with RNA supplied by  
 Wendle lab. Directional cloned into NotI-EV. Clones  
 plated/picked by AGI. More glycerol clones held in -80."
 Query Match 31.7%; Score 516.2; DB 7; Length 858;  
 Best Local Similarity 76.8%; Pred. No. 5.6e-141;  
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 Db |||||  
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Qy 1009 GACGATGAACATGACGAGCTGTATGACATAAGGACTGGTCACCAACTCAAGT---CTAT 1065  
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Db 724 CAGCAACATGGGATAACAGAGTTCCACATGTGACCTCCATGCAATTCCTCAATTTCTGGA 783  
Qy 1126 AGACTTCTTTTCGCTGGCTATGCGAGCAACACACTTGTCTAGTTTGGGATACCCCTCTTG 1185  
Db 784 AGACTTCTTTTCGCGGATACCTC---AAATGGAGATTGCTAGCTATGGGACAGCTTATTG 840  
Qy 1186 GGAGAGGTTGATTGGA 1202  
Db 841 GAAAAGGTCGTTTGA 857

## RESULT 11

CO072054  
LOCUS GR\_Ea31A06.r GR\_Ea Gossypium raimondii cDNA clone GR\_Ea31A06 3',  
mRNA sequence.

ACCESSION CO072054.1 GI:48741535

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Global assembly of Cotton ESTs  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: rwing@genome.arizona.edu  
Plate: 31 row: A column: 06.  
Location/Qualifiers  
1. 871  
/organism="Gossypium raimondii"  
/mol\_type="mRNA"  
/db\_xref="taxon:29730"  
/clone="GR\_Ea31A06"  
/tissue\_type="whole seedlings"  
/dev\_stage="first true leaves"  
/lab\_host="DH10B"  
/clone\_lib="GR\_Ea"  
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:  
EcoRV; Library made by Invitrogen with RNA supplied by  
Wendle lab. Directional cloned into NotI-EV. Colonies  
plated/picked by AGI. More glycerol clones held in -80."

## FEATURES

## source

295 CAGCTCCTCGATACCGATGTGGCGAGGTATTTCAGCGCGCAAGACGTACTCTGGGTGAGC 354  
Db 65 CAGTTGCTCGACACTGATGTTTGTCTACATATGCAAGATCACAAAGGAGAGAGTCCAGTTACT 124  
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Qy 475 ATCGTGTGAATGCTCTAAACGAGTCAGAAACTCATGCTATTAAACTCCCTTTGTCATGG 534  
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Qy 1015 GGAACATGCGAGCTGTATGACATAAGGACTGGTCACCAACTCCAG--GTCTATCAGCCAC 1072  
Db 785 GGAACCTGTAGTTGTTTGACATTTAGAACTGGTCAATTAACAGTATATCTATCAGCAAC 844  
Qy 1073 ATGTTGATGGTGAGAACGGACCTGTCA 1099  
Db 845 ATGGCGATAACGAGGTTCCACATGTGA 871

## RESULT 12

## AI994586

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

AI994586 535 bp mRNA linear EST 08-SEP-1999  
701498643 A. thaliana, Ohio State clone set Arabidopsis thaliana  
cDNA clone 701498643, mRNA sequence.  
AI994586  
AI994586.1 GI:5841491  
EST.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.  
1 (bases 1 to 535)  
Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,

## Query Match

## Best Local Similarity

## Matches

## Conservative

## Indels

## Gaps

## Qy

## Db

## 5

## CAGCGCGCGTACGAGACCGTTAATACCTCCGTGACCACTTATAGACAGAGCGCTC 294

## CAGCGCGCGTACGAGACCGTCAATATCTTAAGAACGATTAAGAAAGAGCTCAA 64

Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzaska,P., Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D., Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C., Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S., Nobrega,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and Hanson,D.

Arabidopsis thaliana Gene Expression Microarray  
 Unpublished (1999)  
 Contact: David Smoller, Ph.D.  
 Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.  
 4633 World Parkway Circle, St. Louis, MO 63134, USA  
 Tel: 877-577-2733  
 Fax: 314-427-3324  
 Email: service@genomesystems.com.

FEATURES  
 source  
 1. 535  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3702"  
 /clone\_lib="A. thaliana, Ohio State clone set"  
 /note="cDNA library was made from selected clones from the Arabidopsis thaliana Ohio State clone set."

ORIGIN  
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 Best Local Similarity 97.6%; Pred. No. 3.7e-140;  
 Matches 521; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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 QY 131 CTCTCTCTCTCTAGACCCCAAAAGTTTCCCTTTTATTGATCGGCGAGAGAGC 190  
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 QY 371 TGGTTTGTGTGCTACTCTTCAGGGACACACCGGAAGGTTTATTATTAGATTGGACAC 430  
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 QY 431 CGGAGGGAACCGGATGTTCAGTGCATCTCAAGATGGGAGATTAATCGTGGGAATGCTC 490  
 Db 361 CGGAGGGAACCGGATGTTCAGTGCATCTCAAGATGGGAGTTCATGTGCGTGGGAATGCTC 420  
 QY 491 TAACGAGTCAGAAACTCATGCTATTAACTCCCTTGTGATGGGTTATGACATGTGCTT 550  
 Db 421 TAACGAGTCAGAAACTCATGCTATTAACTCCCTTGTGATGGGTTATGACATGTGCTT 480  
 QY 551 TCTCTCCAAATGGTCAGTGGTTCGCTGTGGGATTTAGACAGTGTATGTTCTTA 604  
 Db 481 TCTCTCCAAATGGTCAGTGGTTCGCTGTGGGATTTAGACAGTGTATGTTCTTA 534

RESULT 13  
 CO072562 838 bp mRNA linear EST 15-JUN-2004  
 LOCUS GR\_Ea31M19\_r GR\_Ea Gossypium raimondii cDNA clone GR\_Ea31M19 3',  
 DEFINITION mRNA sequence.  
 ACCESSION CO072562

CO072562.1 GI:48742043  
 EST.  
 Gossypium raimondii  
 Gossypium raimondii  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 838)  
 Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and Wing,R.A.  
 Global assembly of Cotton ESTs  
 Unpublished (2004)  
 Contact: Rod A. Wing  
 Arizona Genomics Institute  
 The University of Arizona  
 Forbes Building Room 303, Tucson, AZ, 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: rwing@genome.arizona.edu  
 Plate: 31 row: M column: 19.

FEATURES  
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 /mol\_type="mRNA"  
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 /clone\_lib="GR\_Ea31M19"  
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 /note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2: EcoRV; Library made by invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."

ORIGIN  
 Query Match 31.4%; Score 511.4; DB 7; Length 838;  
 Best Local Similarity 76.2%; Pred. No. 1.5e-133;  
 Matches 629; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

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 Db 185 TCCTTGGATTGGACTCCGGAAGGAAACCGGATTGTTCAGGCGTCTCAGGATCGACGATTA 244  
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 QY 655 AGAATGCTCAGTGGTCACAGGGGATATGTTTCGTGCTGTTCAGTATGTCCCAATAGGAT 714  
 Db 425 AAAACCCCTAGTGGACATAAGGGTTACGCTCTCGTGTGTGTCAGTATGTTCCAGATGAAGAC 484







/tissue\_type="Flavado, albedo, some red scale"  
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/lab\_host="E. coli TJC121"  
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Rind cDNA Library UCRCS11"  
/note="vector: Lambda Uni-ZAP XR, excised phagemid;  
Site\_1: EcoRI; Site\_2: XhoI; In cooperation with Dr.  
Robert Luck and Dr. Joseph Morse, Department of  
Entomology, University of California Riverside, navel  
orange fruit was infested with red scale (Aonidiella  
aurantii [Maskell]). Dr. Luck's technician, Lisa Forster,  
maintained colonies of red scale. Dr. Morse's technician,  
Paul Flores, cleaned and infested the fruit, bagged the  
fruit after the crawlers had time to settle, then  
harvested the fruit at the early second instar and late  
third instar phases of the insect. Claire Federici (Dr.  
Mikeal Roose's lab) cleaned off most of the insects (some  
remained firmly attached), cut the peel, then froze and  
stored at -80°C. The trees used for this set of samples  
were growing in field 16K of the University of California  
Citrus Experiment Station. This was the same field from  
which the tissue was collected for the navel shoot  
meristems and the peel for citrus thrips. Scitrothrips  
citri [Moulton]. The trees were planted 12 October 1992.  
The scion was Parent navel. The trees used for infesting  
with red scale all had troyer rootstock. Three different  
trees were used for each of the two infestations, a total  
of 6 trees. This experiment did not take place according  
to the original schedule because the red scale colony  
became infested with mites, so too few insects were  
available to infest the fruit on the date originally  
planned. The plan had been to infest on or about June 30  
and August 13. Instead the infestation dates were August  
30 and September 27, 2004. Because this took us into the  
cool weather of fall, the insects applied on the second  
infestation date took about three times as long to develop  
to the same stage as the insects applied on the first  
infestation date. The insects were reared on lemons.  
Before infesting the fruit on the trees, Paul Flores  
cleaned the peel and checked to make sure it was not  
already infested. He placed about 200 crawler stage  
insects on the fruit using a soft paintbrush. After the  
crawlers had a day to move around and find a spot to  
attach, Paul placed a very fine mesh drawstring bag over  
the fruit to exclude predators and parasitoids of the  
scale. Bags were left in place for the duration of the  
field development period and also covered control fruit.  
Paul Flores infested fruit on 30 August and 1 September  
2004 after cleaning the fruit on August 27. On 21  
September the first set of red scale infested fruit were  
sampled. He brought Claire Federici 15 infested fruit and  
12 uninfested control fruit. The insects were at the early  
second instar. The controls had been cleaned and bagged at  
the same time as inoculated ones, but had no scale  
introduced. The infestation was heavy, so the insects were  
not well separated on the fruit. A razor blade was used to  
slice off the flavado with about half the thickness of the  
albedo included. The peel from only the stem half of the  
fruit was used because that was where the insects were  
most concentrated. The insects were impossible to wash off  
without severely damaging the peel; each fruit was washed  
with water and a sponge or bottlebrush and wiped dry with  
a paper towel before cutting it, but many of the insects  
were still intact and were included in the sample. The  
pulp had color but the fruit rind was still green. The  
peel from each half fruit was bagged separately in foil  
packets, and pressed between sheets of dry ice to freeze.  
All packets were placed in a paper bag with the date and  
information about 'control' or 'infested', written on the  
bag, and then placed at -80°C. The second sampling date  
from the first infestation was 11 October. Paul brought 19  
infested and 9 uninfested fruit to Claire. These were all  
set up on 30 August. The insects were at the late third

instar. Mikeal Roose's advice was to prepare three bulks  
of each, 5 infested and 3 uninfested fruit per bulk. The  
remaining four infested fruit were infested to a lesser  
degree and were discarded. Washing was done as before and  
the peel from each fruit frozen between sheets of aluminum  
foil pressed between sheets of dry ice. There were quite a  
lot of adhering insects in the frozen rind. After it was  
frozen, the peel from 3 uninfested or 5 infested fruit  
were pooled in a foil packet, then stored at -80°C. The  
pulp had color but the rind was mostly green. However,  
there was a little color developing on some fruit around  
the insects. The third sampling date was 2 December. Paul  
brought the first fruit from the second infestation, which  
were set up on September 27 or 28. He brought 15 infested  
and 10 uninfested fruit. Claire cut and froze them as  
before, making three pools of 5 infested fruit and three  
pools of 3 uninfested fruit. The control fruit all had  
green at the stem end, mostly about 1/4 of the  
circumference from stem to blossom end, but one fruit was  
green all over. The infested fruit were almost fully  
orange, with only a small amount of the surface still  
green, approximately the size of a quarter coin. Paul said  
it would be at least a month, probably 6 weeks or even  
more before the insects reach the late third instar, so  
this was the final sample for the cDNA library due to time  
constraints for EST sequencing. Mandal and Fenton (Close  
lab) purified RNA by the phenol method described in J.  
Japanese Soc. Hort. Sci. 1996. 64 (4): 809-814, purified  
poly(A) mRNA using PolyAT Tract mRNA Isolation Kit  
(Promega), produced a primary cDNA library using a lambda  
ZAP XR cDNA Synthesis Kit (Stratagene), then mass-excised  
1 million pfu from the primary library to produce a  
phagemid population. The library was made from a mixture  
of RNA from each of the three treatments such that  
approximately equal amounts of early second instar and  
late third instar RNA were used. Phagemids were plated,  
plasmid DNA purified, cDNA clones archived, and DNA  
sequences determined bi-directionally using an ABI3730 at  
the Arizona Genomics Institute (Kim, Kudrna, Collura,  
Wisotaki, Byrne, Stum, Smart, Muller, Wing). Chromatogram  
files were downloaded by FTP by Close, then processed by  
Wanamaker (Close lab) using the HarVest pipeline  
(http://harvest.ucr.edu) to remove vector and cloning  
oligo sequences and various contaminants, and to trim to a  
high quality region. Sequences that retained a phred 17  
region of at least 100 bases were assembled, then chimeras  
were removed following manual inspection of assemblies  
(Wanamaker, Close, Roose). Sequences that survived all  
removal steps were submitted to GenBank. Clones from this  
library are archived at the Arizona Genomics Institute  
(http://www.genome.arizona.edu/orders/).

## ORIGIN

Query Match	31.0%	Score 504.6;	DB 8;	Length 778;
Best Local Similarity	79.1%;	Pred. No. 1.5e-137;		
Matches 613;	Conservative 0;	Mismatches 159;	Indels 3;	Gaps 1;
QY	325	TCAGCGGCGCAAGGACGTACTCGGGTGAGCTTCGGAGCAACGGATCTGTTTGTGCT	384	
Db	4	TCGAGGTCGACGGGTGGGCTCCGGTCAGCTTGGTCCGACCGATCTAGTTGTTGAGG	63	
QY	395	ACTCTTCAGGGACACACCGGAAAGGTTTATTCATTAGATTGGACACCGGAGGACCGG	444	
Db	64	ACCTTGCAGGCGCACGCTGGCAAGGTATATTCATTGGACTGGACTTCCGAAAGGAATCGA	123	
QY	445	ATTGTGCTGTCATCTCAAGATGGGAGATTATTCGTGTGGAATGCTCTCAACAGTCAAGAA	504	
Db	124	ATTGTGCTGTCATCTCAAGATGGGAGATTATTCGTGTGGAATGCTCTCAACAGCAGAA	183	
QY	505	ACTCATGCTATTAAACTCCCTTGTGCATGGGTTATGACATGTGCTTCTCTCCAATGCT	564	
Db	184	ACTCATGCTATTAAACTGCTTGTGCTGGGTAATGACTTGTGCTTCTCTCCAATGCT	243	

QY	565	CAGTCGGTTGCGTGTGGATTAGACAGTGATGTTCTATCTTTAGCCTTAGCTCAACG	624
Db	244	CAATCTGTGCGTGTGGTCTTGATAGTGTTCCTCCATTTCAACCTGAATCTCCT	303
QY	625	GCGGACAAAGGATGGAACGTGTACCGGTTTCAAGAACTCTACCTGGTCACAGGGGATATGTT	684
Db	304	ACTGACAAAGGACGGGAATTTACAGTATCAAGATGCTTAGTGGGCACAAGGGTTATGTG	363
QY	685	TCGTGCTGTCAGTATGTCCCAAAATGAGGATGCCACCTTATCACCAGTTTCAGGTGATCAA	744
Db	364	TCCTGCTGTCAGTATGTTCTTGATGAGGACACTCACCTAAATTACAGTTTCAGGTGACCAA	423
QY	745	ACTTGTATCTTATGGGATGTAACACTACTGGTCTCAAAACTTCTGTTTTTGGCGGTGAATTT	804
Db	424	ACCTGTGTTTTTGGGATATTACTACAGGCCCTTAGAACTTCTGTTTTTGGAGGAAATTT	483
QY	805	CAGTCTGGACATACCTGCTGATGTACTAAGCGTCTCAATCAGTGGATCAAACTCAACTGG	864
Db	484	CAGTCTGGGCACACTGCTGATGTGTTAAGTGTCTCAATAGTGGTTCAAACTCAAGGATG	543
QY	865	TTTATATCTGGTTTCATGCGATTCCACAGCAGCGTTGTGGGACACTCGTGTGCAAGCCGA	924
Db	544	TTTGTGTCGTGTTCTGTGATTCTACTGCCGATTGTGGGATCTCGTGTGCAAGTCGA	603
QY	925	GCAGTGGTACCTTTTCATGGTTCACAGGGAGATGTTAATACGGTCAAGTTCTTTCCGGAT	984
Db	604	GCAGTGGCCACATTTTCATGGGCATGAGGGAGATGTTAACTGTGAAGTTCTTTCCAGAT	663
QY	985	GGGTATAGATTTGGGACTGGATCAGACGATGGAACATGCAGCTGTATGACATAGGACT	1044
Db	664	GGCAATAGTTTGGAACTGGCTCAGACCATGGAACTTGCAATTAATTTGATATCAGGACT	723
QY	1045	GGTCACCAACTCCAGGT---CTATCAGCCACATGGTGTATGGTGAGAACGGACCTG	1096
Db	724	GGGCACCAACTCCAGTGTATTATCAGCAGCACGCGTGAGAAATGAGATCCACATG	778

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 Job time : 5985 secs

GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2005, 14:53:47 ; Search time 319 Seconds  
(without alignments)  
9077.266 Million cell updates/sec

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Perfect score: 1629  
Sequence: 1 cctgacgtacgcgtgttg.....cagaagataaaacgtacta 1629

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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8: /cgn2\_6/prodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/prodata/1/ina/backfileseq.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130	8.0	1520	3	US-09-492-029-2
2	110.8	6.8	1523	3	US-09-803-653-1
3	110.8	6.8	1523	3	US-09-492-029-4
4	109.4	6.7	3078	3	US-09-949-016-1956
5	109.4	6.7	3088	3	US-09-023-655-1294
6	109.2	6.7	1517	3	US-09-180-783-1
7	109.2	6.7	1523	3	US-09-803-653-2
8	107.8	6.6	1542	3	US-09-949-016-1365
9	96	5.9	894	3	US-09-803-653-4
10	83.8	5.1	1394	3	US-09-147-826B-1
11	71.4	4.4	2119	3	US-09-032-372-6
12	61	3.7	659	3	US-09-016-434-1017
13	58.2	3.6	551	3	US-09-270-767-53
14	58.2	3.6	551	3	US-09-270-767-53
15	52.8	3.2	110243	3	US-09-949-016-13698
16	51.8	3.2	1215	3	US-09-248-796A-6112
17	50.6	3.1	7218	2	US-08-232-463-14
18	44.8	2.8	7218	2	US-08-232-463-14
19	44.2	2.7	9308	3	US-09-949-016-13107
20	42.8	2.6	2359	2	US-08-188-582-4
21	42.8	2.6	2359	2	US-08-646-715-4
22	42.4	2.6	1422	3	US-09-248-796A-4567
23	41	2.5	48682	3	US-09-949-016-17236
24	41	2.5	48682	3	US-09-949-016-17237

C 25	41	2.5	48682	3	US-09-949-016-17238	Sequence 17238, A
C 26	41	2.5	48682	3	US-09-949-016-17239	Sequence 17239, A
C 27	41	2.5	51022	3	US-09-949-016-17135	Sequence 17135, A
C 28	41	2.5	51022	3	US-09-949-016-17136	Sequence 17136, A
C 29	41	2.5	51022	3	US-09-949-016-17137	Sequence 17137, A
C 30	41	2.5	51022	3	US-09-949-016-17138	Sequence 17138, A
C 31	41	2.5	86213	3	US-09-949-016-17240	Sequence 17240, A
C 32	41	2.5	86213	3	US-09-949-016-17241	Sequence 17241, A
C 33	41	2.5	86213	3	US-09-949-016-17242	Sequence 17242, A
C 34	41	2.5	86213	3	US-09-949-016-17243	Sequence 17243, A
C 35	40	2.5	1761	3	US-09-949-002-268	Sequence 268, App
C 36	40	2.5	1766	6	PCT-US93-00601-1	Sequence 1, Appl
C 37	40	2.5	1766	6	PCT-US94-07107A-1	Sequence 1, Appl
C 38	40	2.5	1766	6	PCT-US94-07107A-1	Sequence 1, Appl
C 39	40	2.5	1767	3	US-08-083-945C-1	Sequence 1, Appl
C 40	40	2.5	52202	3	US-09-949-016-17006	Sequence 22, Appl
C 41	39.8	2.4	1141	3	US-10-071-411A-63	Sequence 63, Appl
C 42	39.6	2.4	168174	3	US-10-071-411A-2	Sequence 2, Appl
C 43	39.6	2.4	168273	3	US-10-071-411A-2	Sequence 2, Appl
C 44	39.2	2.4	152331	3	US-09-128-155-16	Sequence 16, Appl
C 45	39.2	2.4	176373	3	US-09-128-155-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1  
US-09-492-029-2  
; Sequence 2, Application US/09492029  
; Patent No. 6929925  
; GENERAL INFORMATION:  
; APPLICANT: Zuker, Charles S.  
; APPLICANT: Adler, Jon Elliot  
; APPLICANT: Lindemeier, Juergen  
; APPLICANT: The Regents of the University of California  
; APPLICANT: Assays for Sensory Modulators Using a Sensory Cell  
; TITLE OF INVENTION: Specific G-Protein Beta Subunit  
; FILE REFERENCE: 02307E-092710US  
; CURRENT APPLICATION NUMBER: US/09/492,029  
; CURRENT FILING DATE: 2000-01-26  
; PRIOR APPLICATION NUMBER: US 60/117,404  
; PRIOR FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; TYPE: DNA  
; ORGANISM: Rattus sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (78)..(1097)  
; OTHER INFORMATION: rat taste cell specific G-protein beta 3 subunit  
; OTHER INFORMATION: (TC-Gbeta3)  
US-09-492-029-2

Query Match	8.0%	Score 130;	DB 3;	Length 1520;
Best Local Similarity	52.8%	Pred. NO. 8e-32;		
Matches	501;	Conservative	0;	Mismatches 390;
Indels	57;	Gaps	8;	
QY	383	GTACTCTTCAGGACACACCGGAAGTTTATTTCATTAGATTGGACACCGGAGGAGAAC	442	
Db	223	GGACGTTTAGGGACACCTGGCTAAGATCTATGCCATGCACTGGGCACTGACTCTTAGC	282	
QY	443	GGATTGTCACTGATCTCAAGATGGGAGATTATTCGTGGATGCTCTAACGAGTCAGA	502	
Db	283	TGCTAGTAACTGCTCGAGGATGGGAGCTGATCGTGTGGGACATTACACCAATA	342	
QY	503	AACTCATGCTATTAACTCCCTTGTGCTGATGGGTTATGACATGCTCTTCTTCCAATG	562	
Db	343	AGTGATGCTATCCCGCTCGCTTCCTCTCGGCTCATGACCTGCTGCTATGCACCATCAG	402	
QY	563	GTCACTGGTGGTGGTGGGATTAGACAGTGTATGTTCTATCTTTAGCTTTAGCTTCA	622	

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Qy 623 CGGCGGAAGAAGATGGAATCTGTACCGTTTCAAGAATGCTCACTGGTCACAGGGGATATG 682
Db 461 -----CGTGAGGCAATGTCAAGGTGAGCGCGGAACCTCTCGGCTCACAGGTTATC 513
Qy 683 TTTCTGTCTGATGATGTCCCAATGAGGATGCCACCTTATACACGATTCAGGTGATC 742
Db 514 TCTCTGTGTCCGCTTCCT-----GGATGACAACAACATTTGTGACTAGCTCTGGGACA 567
Qy 743 AAATTTGATCTTATGGGATGTAATCTACTGTGCTCAAAATTTCTGTTTGGCGGTGAT 802
Db 568 CCACTGTGCTTGTGGACATGTAGACGGGCGAGAGACAGTGTTCG----- 618
Qy 803 TTCAGTCTGGACATCTGCTGATGTAATAAGCGTCTCAATCAGTGGATCAAAACCCAAACT 862
Db 619 -----TGGGACACACTGTGTACTGATGAGCTGCTGCT---GTCCCGAGACTACAAAC 669
Qy 863 GGTTTATATCTGGTTCATGCGATTCACAGCAGCGTTGTGGACACTCGTGTGCAAGCC 922
Db 670 TCTTCATCTCGGGAGCTTGTGATGCGCAGCGCCAAGCTCTGGGATGTGAGGGAAGGGAAGCT 729
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Qy 1103 CCATTTGCAATCTCTGTGTCAGGAGACTTCTTTTCGCTGGCTATCGAGCAACAACACTT 1162
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Qy 1163 GCTACGTTTGGGATACCTCTTTGGGAGAGTTGTATTTGGATTGGGATTACAGCAGGAT 1222
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Qy 1223 CACACAGGAATAGATAGCTGTTTGGGGTTGTACAGAGATGGAAGTGCATGTGTACAG 1282
Db 1006 GCCATGACAACAGAGTCAAGTTCCTCGGGGTACAGCTGACGSCATGGCTGTGGCACTG 1065
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## RESULT 2

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US-09-803-653-1
; Sequence 1, Application US/09803653
; Patent No. 6924100
; GENERAL INFORMATION:
; APPLICANT: Sifert, Winfried
; TITLE OF INVENTION: GENE ALTERATION IN THE GENE FOR THE GBETA3-SUBUNIT OF THE HUMAN G
; FILE REFERENCE: 741135-12
; CURRENT APPLICATION NUMBER: US/09/803,653
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: PCT/EP99/06534
; PRIOR FILING DATE: 1999-09-06
; PRIOR APPLICATION NUMBER: DE 198 41 299.1
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: DE 199 04 825.8
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: DE 199 12 049.8
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: DE 199 14 229.7
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: DE 199 19 989.2
; PRIOR FILING DATE: 1999-04-30
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; PRIOR APPLICATION NUMBER: DE 199 23 539.2
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-803-653-1
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## Query Match 6.8%; Score 110.8; DB 3; Length 1523;

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Best Local Similarity 51.3%; Pred. No. 1.9e-25;
Matches 495; Conservative 0; Mismatches 412; Indels 57; Gaps 8;
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Qy 380 GTCGTACTCTTTCAGGGACACACCGAAAGGTTTATTATTAGATTGGACACCGGAGGA 439
Db 149 GCGGACGTTAAGGGGACACCTGCGCAAGATTTCAGCCATGCACTGGCCACTGATTCTA 208
Qy 440 ACCGATTTGTCAGTGCATCTCAAGATGGGAGATTAAATCGTGTGGAATGCTCTAAAGATC 499
Db 209 AGCTGCTGGTAAGTGCCTCGCAAGATGGAAAGCTGATCGTGTGGACAGCTACACCA 268
Qy 500 AGAAACTCATGCTATTAAACTCCCTTGTGATGGGTTATGACATGCTTCTCTCAA 559
Db 269 ACAAGGTGCACGCCATCCCACTGCGCTCCTCTGGGTCATGACCTGTGCTATGCCCAT 328
Qy 560 ATGTCAGTCCGTTGCGTGTGGTGTAGACAGTGTATGTTCTTATCTTTAGCCCTTAGCT 619
Db 329 CAGGNACTTTGTGCGATGTGGGGGCTGGACAACATGTTTCCATCTACAACTCAAT 388
Qy 620 CAACGGCGGACAAGGATGGAATCTGACCGGTTTCAAGAAATGCTCACTGGTCACAGGGAT 679
Db 389 C-----CCGTGAGGGCAATGTCAAGGTGAGCGGGAGCTTTCTGCTCACAGGTT 439
Qy 680 ATGTTTCGTGCTGTCAGTATGTCCTCCAAATGAGGATGCCACCTTTATCACAGTTCAAGTG 739
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Qy 740 ATCAAACTTTGATCTTATGGGATGTAACTACTGCTCTCAAAACTTCTGTTTTTGGCGGTG 799
Db 494 ACACCACTGTGCTTGTGGACATTTGAGACTGGGCGAGCAGAACTGATTG----- 547
Qy 800 AATTTAGTCTGGACATACCTGCTGATGTATTAAGCGTCTCAATCAGTGGATCAAAACCAA 859
Db 548 -----TGGGACACACGGGTGACTGCAATGAGCTGGCTGTGTCT---CCTGACTCA 595
Qy 860 ACTGTTTATATCTGTTTCATGCGATTCACAGACCGGTTGTGGGACACTCGTGTCTCAA 919
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Qy 980 CGGATGGGTATAGATTTGGGACTCGATCAGACGATGGAACATGAGGCTGTATGACATAA 1039
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Qy 1040 GGACTGGTCAACCAACTCCAGTCTATCAGCCACATGTTGATGTTGAGAACCGACCTGTCA 1099
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 DB 1052 GAAG 1055

RESULT 3  
 US-09-492-029-4  
 ; Sequence 4, Application US/09492029  
 ; Patent No. 6929925  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zuker, Charles S.  
 ; APPLICANT: Adler, Jon Elliot  
 ; APPLICANT: Lindemeier, Juergen  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: Assays for Sensory Modulators Using a Sensory Cell  
 ; FILE REFERENCE: Specific G-Protein Beta Subunit  
 ; CURRENT APPLICATION NUMBER: US/09/492,029  
 ; CURRENT FILING DATE: 2000-01-26  
 ; PRIOR APPLICATION NUMBER: US 60/117,404  
 ; PRIOR FILING DATE: 1999-01-27  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 1523  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (7)..(1029)  
 ; OTHER INFORMATION: human taste cell specific G-protein beta 3 subunit  
 US-09-492-029-4

Query Match 6.8%; Score 110.8; DB 3; Length 1523;  
 Best Local Similarity 51.3%; Pred. No. 1.9e-25;  
 Matches 495; Conservative 0; Mismatches 412; Indels 57; Gaps 8;  
 QY 380 GTGCTACTCTTACGGACACACCGGAAAGTTTATTCATTAGATTGGACACCGGAGAGA 439  
 DB 149 GCGGACGTTAAGGGACACCTGCGCAAGATTTACGCCATGCACTGGGCCACTGTCTA 208  
 QY 440 ACCGATTGTGCTGATCTCAAGATGGGAGATTAATCGTGTGAATGCTCTAACGATC 499  
 DB 209 AGCTGCTGAAGTGCTGCAAGATGGGAGCTGATCGTGTGGACAGCTACACCA 268  
 QY 500 AGAAACTCATGCTATTAACTCCCTTGTGTCATGGGTTATGACATGCTTTCTCCAA 559  
 DB 269 ACAAGTGCAAGCCATCCCACTGGCTCTCTGCTGGTCAATGACCTGTGCTATGCCCAT 328  
 QY 560 ATGCTAGTCGGTGTGGTGGATAGACAGTGTATGTTCTATCTTTAGCTTAGCT 619  
 DB 329 CAGGAACTTTGTGGCATGTGGGGGCTGGACAACATGTGTTCCATCTACAACCTCAAT 388  
 QY 620 CAACGGCGGACAGGATGGAATGTACCGGTTTCAAGATGCTCACTGGTCAACGGGAT 679  
 DB 389 C-----CCGTGAGGGCAATGTCAAGTCAAGCGGGAGCTTTCTGCTCACACAGTT 439  
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 DB 440 ATCTCTCTGCTGCGCTTCT-----GGATGACAACATATGTCACAGCTCGGGG 493  
 QY 740 ATCAACTTGTATCTTATGGATGTAACTACTGCTCTCAAACTCTGTTTGGGGG 799  
 DB 494 ACACCACTGTGCTTGTGGGCAATGAGACTGGGACGAGAAGCTGTATTTG----- 547  
 QY 800 AATTTCAGTCTGGACATCTGCTGATGATTAAGCGTCTCAATCAGTGGATCAAAACCA 859  
 DB 548 -----TGGGACACACGGGTGACTGCAATGAGCTTGGCTGTGCTCT---CCTGACTTCA 595

QY 860 ACTGTTTATATCTGTTTCATGCGATTCACAGCACCGTTTGGGACACTCGTGTGCAA 919  
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 QY 1100 CTTCCATTGCAATCTCTGTCAGGAGACTTTCTTTTCGCTGGCTATGCGAGCAACAACA 1159  
 DB 827 GTGCTGGCTTCTTCTCTCAGTGGCGCTTACTTATTCGCTGCTACGACGACTTCAAC- 885  
 QY 1160 CTTGCTACGTTTGGGATACCTCTTTGGGAGAGTTGTTATGATTTGGGATTACAGCAGG 1219  
 DB 886 --TGCATGCTGGGACTCCATGAAGTCTGAGCGTGTGGGCATCTCTC----- 932  
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 QY 1280 CAGGAGTTGGGATTTCAAAATCTAAAGATATGGCGCTTTGGAGGACACAGGAGAGTAT 1339  
 DB 992 CAGGTTCTTGGGACAGCTTCTCAAAATCTGGAATCTGAGAGGCTGGAGAAAGGAGTG 1051  
 QY 1340 GAAG 1343  
 DB 1052 GAAG 1055

RESULT 4  
 US-09-949-016-1956  
 ; Sequence 1956, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1956  
 ; LENGTH: 3078  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-1956

Query Match 6.7%; Score 109.4; DB 3; Length 3078;  
 Best Local Similarity 51.8%; Pred. No. 8.7e-25;  
 Matches 481; Conservative 0; Mismatches 391; Indels 57; Gaps 8;  
 QY 383 GTACTCTTACGGACACACCGGAAAGTTTATTCATTAGATTGGACACCGGAGAGAAC 442  
 DB 425 GGACACTGGGGGCGACCTTGGCCAGATCTACGCCATGCACTGGGCAACAGACTCCAGC 484  
 QY 443 GGATTTCTAGTGCATCTCAAGATGGGAGATTAATCGTGTGAATGCTCTTAACGAGTCA 502

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Db 485 TTCTCGTCAGTCCCTCGCAGGATGTTAACTTATCATCTGGGACAGCTACACCAACA 544
Qy 503 AAACATCATGCTATTAACTCCCTTGTGCAATGGGTTATGACATGTTCTCTCCAAATG 562
Db 545 AGGTCCAGCCATCCCTCTCGCTCTCTCGGTCATGACCTGTGCATATGCCCTTCTG 604
Qy 563 GTCACTCGGTCGGTGTGGTGTGAATAGACAGTGTATGTTCTATCTTTAGCTTACGTCAA 622
Db 605 GGAACATATGTGCGCTCGCGTGGCTGGATAACATTTGCTCCATTTACATCTGAAAC-- 662
Qy 623 CGGCGGACAAGATGGAATGTAACCGGTTTCAAGATGCTCACTGTCACAGGGGATATG 682
Db 663 -----TCGTGAGGGGAACGTGCGGTGAGTCGTGAGCTGGCAGACACAGGTTACC 715
Qy 683 TTTCGTGCTGTGTCAGTATGTCCCAATAGAGATGCCACCCTTATCACCAAGTTCAGGTGATC 742
Db 716 TGTCTGCTGCTCGGATTCCT-----GGATGACAATCAGATCGTCAACAGCTCTGGAGCA 769
Qy 743 AAACCTGTATCTTATGGGATGTAACATCTATGCTCTCAAACTTCTGTTTGGCGGTGAAT 802
Db 770 CCACGTGTGCTGCTGTGGGATCGAGACCGGCGCAGCAGCAGCACGCTTT-----819
Qy 803 TTCAGTCTGGACATCTGCTGATGTAAGAGTCTCAATCAGTGTGATCAAACTCAAACT 862
Db 820 -----ACGGACACACTGGAGATGATAGGCTTTCTCT---TGCTCTGACACAGAC 871
Qy 863 GGTATTATCTGTTTCATGCGATTCACAGCAGCGTGTGGGACACCTGCTGCTGCAAGCC 922
Db 872 TGTCTGCTCTGCTGTGATGCTTCTAGCAAACTCTGGATGTGCG---AGAGGCA 928
Qy 923 GAGCAGTGGTACCTTTTCATGTCAGGAGGAGATGTTAATACGGTCAAGTTCTTTCCGG 982
Db 929 TGTGCGCGCAGACCTTCACTGGCCACGAGTCTGACATCAATGCCATTTGCTTTTCCAA 988
Qy 983 ATGGGTATAGATTTGGGATGATGACAGATGAGGATGACAGCTGTATGATGATGATGATG 1042
Db 989 ATGGCAATGATTTGCACTGTGCTGACAGCAGCCACCTGCAAGCTGTGTTGACCTTCG 1048
Qy 1043 CTGGTCACCACTCCAGGCTTATACGCCACATGCTGATGGTGAGAACCGGACCTGCACCT 1102
Db 1049 CTGACCAAGGCTCATGACTTACTCC-----ATGACAACATCATCTGCGGGATCACT 1102
Qy 1103 CAATTGCAATCTGTGTCAGGAGACTTTCTTTTCTGGCTATGCGAGCAACAACTT 1162
Db 1103 CTGTCTCTCTTCCAGAGCGGCGCTCTCTCTGCTGGGTACG---ACGACTTCAACT 1159
Qy 1163 GCTAGTTTGGGATACCTCTTTGGGAGAGGTTGATTTGGATTTGGATTTACAGCAGGAT 1222
Db 1160 GCAAGCTCTGGATGCACTCAAGCGGACCGGCGCAGGTGCTTT-----GGCTG 1207
Qy 1223 CACACAGGAATAGAATAGCTTTTGGGTTGTGACAGATGGAAGTGCATTTGTGTACAG 1282
Db 1208 GGCATGACAAACCGCTCAGCTGCTGGGCTGACTGACGATGCGATGCTGCTGGCGACG 1267
Qy 1283 GAAGTTGGGATCAAACTTAAGATATGG 1311
Db 1268 GGTCTGGGATAGCTTCTCTCAAGATCTGG 1296

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RESULT 5
US-09-023-655-1294
; Sequence 1294, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE

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; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1294:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3088 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 931667
; US-09-023-655-1294

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Query Match 6.7%; Score 109.4; DB 3; Length 3088;
Best Local Similarity 51.8%; Pred. No. 8.8e-25;
Matches 481; Conservative 0; Mismatches 391; Indels 57; Gaps 8;

Qy 303 GTACTCTTCAGGGACACACCGGAAGGTTTATTATTAGATTGGACACCGGAGGAAACC 442
Db 426 GGACACTCGGGGGACCTGGCCAAAGATCTAGCCATGCACTGGGGCAACAGACTCCAGGC 485
Qy 443 GGATTGTCACTGTCATCTCAAGATGGGAGATTAATCGTGTGGAATGCTCTAACGAGTCAGA 502
Db 486 TTCCTGTCAGTGCCTCGCAGGATGTTAACTTATCATCTGGACAGCTACACCAACA 545
Qy 503 AAACATCATGCTATTAAACTCCCTTGTGTCATGGGTTATGACATGCTTTCTCTCAAAATG 562
Db 546 AGGTCCACGCCATCCCTCTGCGCTCCTCTGGGTCAAGACCTGTGCATATGCCCTTCTG 605
Qy 563 GTCACTCGGTTGCGTGTGGTGTAGACAGTGTATGTTCTATCTTTAGCCTTAGCTCAA 622
Db 606 GGAATATGTGGCTTGGCTGGCTGGATAACATTTGCTCTCAATTTACATCTGAAAC-- 663
Qy 623 CGGCGGACAAGGATGGAATGTAACCGGTTTCAAGAAATGCTCACTGCTCACAGGGGATATG 682
Db 664 -----TCGTGAGGGGAACGTGCGGTGAGTCGTGAGCTGGCAGGACACAGGTTACC 716
Qy 683 TTTCTGTCGTGTCAGTATGTCCTCAAAATGAGGATGCCCCACCTTATCACCAAGTTCAGGTGATC 742
Db 717 TGTCTGCTGCGGATTCCT-----GGATGACAATCAGATCGTCAACAGCTCTGGAGACA 770
Qy 743 AAACCTGTATCTTATGGGATGTAACCTACTGCTCTCAAACTTCTGTTTTCGGCGGTGAAT 802
Db 771 CCAGTGTGCGCTGTGGGACATCGAGACCGGCCAGCAGACACCACTGTT-----820
Qy 803 TTCAGTCTGGACATCTGCTGATGATCTAAGCGCTCTCAATCAGTGGATCAAACTCAAACT 862
Db 821 -----ACGGACACACTGGAGATGTCATGAGCCCTTCTCT---TGCTCTGACACAGAC 872
Qy 863 GGTATTATCTGGTTTCATGCGATTCACAGACCGGTTGTGGGACACTGCTGCTGCAAGCC 922

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[illegible]

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RESULT 7
US-09-803-653-2
; Sequence 2, Application US/09803653
; Patent No. 6924100
; GENERAL INFORMATION:
; APPLICANT: Sifert, Winfried
; TITLE OF INVENTION: GENE ALTERATION IN THE
; FILE REFERENCE: 741135-12
; CURRENT APPLICATION NUMBER: US/09/803,653
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: PCT/EP99/06534
; PRIOR FILING DATE: 1999-09-06
; PRIOR APPLICATION NUMBER: DE 198 41 299.1
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: DE 199 04 825.8
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: DE 199 12 049.8
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: DE 199 14 229.7
;

```

	Query Match	6.7%;	Score 109.2;	DB 3;	Length 1517;
	Best Local Similarity	51.2%;	Prod. No. 6.3e-25;		
	Matches 494;	Conservative	0;	Mismatches 413;	Indels 57; Gaps 8;
Qy	380	GTGCTACTCTTCAGGGACACACCGGAAGGTTTATTCAATAGATTGGACACCGGAGGGA	439		
Db	143	GGCGGACCTTAAGGGGACACCTGGCCAGATTTACGCCATGCATCTGGGCCACTGATTCTA	202		
Qy	440	ACCGGATTGTCAGTGCACTCTCAAGATGGGAGATTAAATCGTGTGGAATGCTCTTAACGAGTC	499		
Db	203	AGCTGCTGGTAAGTGCTTCGCAAGATGGGAAGCTGATCGTGTGGGACAGCTACACCCACA	262		
Qy	500	AGAAACTCATGCTATTAAATCCCTTGTCATCGGTTATGACATGTGCTTTCTCTCCAA	559		
Db	263	ACAAGGTGACGCCATCCCACTCGCGCTCCTCTCGGCTCATGACCTGTGCGCTATGCCCCAT	322		
Qy	560	ATGGTTCAGTCGGTGTGCTGGATTAGACAGTGTATGTTCTATCTTTAGCCCTTAGCT	619		
Db	123	CAGGGAACTTTGTGCACTGTGGGGGCTGGCAACATGTTTTCATCTACAACTCAAT	382		

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; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: DE 199 19 989.2
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: DE 199 23 539.2
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-803-653-2

Query Match      6.7%; Score 109.2; DB 3; Length 1523;
Best Local Similarity 51.2%; Pred. No. 6.3e-25;
Matches 494; Conservative 0; Mismatches 413; Indels 57; Gaps 8;

QY 380 GTCGTACTCTTCAGGGACACACCGGAAGGTTATTTCATTAGATTGGACACGGAGAGA 439
Db 149 GCGGACGTTAAGGGACACCTGGCCAAAGATTTACGCCATGCACCTGGGCCACTGATCTTA 208
QY 440 ACCGGAATGTCAGTGCATCTCAAGATGGAGATTAACTCTGTGGAAATGCTCTTAACGAGTC 499
Db 209 AGCTGCTGTAAGTGCTCGCAAGATGGAGCTGATGCTGTGGACAGCTACACCA 268
QY 500 AGAAACTCATGCTATTAACCTCCCTTGTGCATGGTTATGACATGTGCTTTCTCTCAA 559
Db 269 ACAAGGTGACGCCATCCCATCGCTCTCTCGGTGATGACCTGTGCTATGCCCCAT 328
QY 560 ATGTCAGTCGGTTGCGGTGTGTGATTTAGACAGTGTATGTTCTATCTTTAGCCTTAGCT 619
Db 329 CAGGGAACCTTTGTGCACTGTGGGGGCTGGCAACATGTGTTCCATCTACAACTCAAT 388
QY 620 CAACGGGGACAAAGATGGAATGTACCGGTTTCAAGAAATGCTCACTGTGCACGGGAT 679
Db 389 C-----CGTGAGGCAATGTCAAGTTCAGCGGGAGCTTCTGCTCACAGGTT 439
QY 680 ATGTTTCGTGCTGTCAGTATGTCCTCAATAGAGATGCCACCTTATCAACAGTTTCAGGTG 739
Db 440 ATCTCTCTGCTGCGGCTTCTCT-----GGATGACAAACAATATTTGTGACCACTCGGGG 493
QY 740 ATCAAACTGTATCTTATGGGATGTAATCACTGCTGCTCAAACTTCTGTTTTCGGGTG 799
Db 494 ACACCAGCTGTGCTTGTGGGACATTTGAGACTGGGACGACGAGAAGACTGTATTTG----- 547
QY 800 AATTTTCAGTCTGGACATATCTGCTGATGTACTAAGCGTCTCAATCAGTGGATCAAAACCCA 859
Db 548 -----TGGGACACACGGGTGACTGCATGAGCTGGCTGTCTCT---CTGACTTCA 595
QY 860 ACTGTTTATATCTGGTTCAATCGGATTCACAGCAGGTTGTGGACACTCGTGTCTGCAA 919
Db 596 ATCTCTTCAATTTCCGGGGGCTGTGATGTCAGTGCACCAAGCTCTGGGATGTGCGAGAGGGA 655
QY 920 GCCAGCAGTCGCTACCTTTCATGCTCAGGGAGATGTTAATACGCTCAAGTTCTTTC 979
Db 656 CTTG---CCGTGAGACTTTCACTGSCCAGAGTCGGACATCAACCCCATCTGTTTCTTCC 712
QY 980 CGGATGGGTATAGATTTGGGACTGGATCAGACGATGGAACTGAGGCTGTATGACATAA 1039
Db 713 CCATGGAGAGGCCATCTGCAGGGCTCGEATGACGCTTCTCGCGCTGTTTGGACTCG 772
QY 1040 GGAATGGTCAACAACTCAGGCTTATCAGCCACATGGGTGATGGTGAAGAACGGACCTGCA 1099
Db 773 GGGCAGACAGGAGCTGATCTGCTTCTCC-----ACGAGAGCATCATCTGCGGCATCA 826
QY 1100 CCTCCATTTGCAATCTGCTGTGAGGAGACTTCTTTTCGCTGGCTATGGAGCAACA 1159
Db 827 GGTCTGTGGCTTCTTCCCTCAGTGGCGGCTACTATTCGCTGGCTACGACGACTTCAAC- 885
QY 1160 CTTGTACGTTTGGGATACCTCTTTGGGAGAGGTTGATTTGGATTTGGGATTTACAGCAGG 1219
Db 886 --TGCAATGTCTGGGACTCCATGAAATCTGACCGCTGTGGGCATCTCTC----- 932
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QY 1220 ATTCACACAGGAATAGAAATAGCTGTTTGGGTTGTGTCAGCAGATGGAAGTGCATTGTGTA 1279
Db 933 -TGGCCACGATAACACAGGGTGAGCTGCTCTGGAGTCAACAGCTGACGGGATGCTGTGGCCA 991
QY 1280 CAGGAAGTTGGGATTCAAATCTAAGATATGGGGCTTTGGAGGACACAGGAGAGTATTT 1339
Db 992 CAGGTTCCTGGGACAGCTTCTCAAATCTGGAATCTGGAATCTGAGGAGGCTGGAGAAAGGAAGTG 1051
QY 1340 GAAG 1343
Db 1052 GAAG 1055

RESULT 8
US-09-949-016-1365
; Sequence 1365, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1365
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1365

Query Match      6.6%; Score 107.8; DB 3; Length 1542;
Best Local Similarity 51.7%; Pred. No. 1.8e-24;
Matches 480; Conservative 0; Mismatches 392; Indels 57; Gaps 8;

QY 383 GTACTCTTCAGGGACACACCGGAAAGGTTTATTCATTAGATTGGACACCGGAGAGGAACC 442
Db 298 GGACCCCTCCGTGGGCACCTGGCAAGATCTATGCGATGCACTGGGGGACCGCACTCAAGGC 357
QY 443 GGATTGTGAGTCACTCAAGATGGAGATTAATCGTGTGAATGCTCTACAGATCAGA 502
Db 358 TGCTGGTTCAGCGCTCCAGGATGGGAGCTCATCATCTGGGACAGCTACACCCACCAACA 417
QY 503 AAACCTCATGCTATTAAACTCCCTTTGTGATGGGTTATGACATGTGCTTTCTTCCAAATG 562
Db 418 AGGTCCAGCCATCCCGCTCGCTCTCTGGGTAATGACCTGTGCTTACCGGCCCTCAG 477
QY 563 GTCAGTCGGTTGCGTGTGGATTAGACAGTGTATGTTCTATCTTTAGCCTTAGCTCAA 622
Db 478 GGAACCTTGTGGCCTGTGGGGGTTGGACAAATCTGCTCCATCTACAGCCTCA----- 531
QY 623 CGGCGGACAGGATGGAACCTGACCGGTTTCAAGAAATGCTCACCTGCTCAGAGGGGATG 682
Db 532 ---AGACCCGCGAGGGAACCGTCAGGGTTCAGCCGGAGCTGCCCTGGCCACACTGGGTACC 588
QY 683 TTTGCTGCTGTCAGTATGTCCTCAAAATGAGGATGCCACCTTATCACCAGTTTCAGTGTATC 742
Db 589 TGTGCTGTGCGCTTCTCT-----GGATGACAAACCAATCATCACAGCTCTGGGATA 642
QY 743 AAACCTGTATCTTATGGGATGTAATCTACTGTGCTCAAAACTTCTGTTTTCGGCGGTGAAT 802
Db 643 CCACCTGTGCGCTGTGGGACATTTGAGACAGGCCACGAGCAGACAGTGGGTTTTTTC----- 693
QY 803 TTCAGTCTGGACATCTGCTGATGCTACTTAAGCGTCTCAATCAGTGGATCAAAACCAACT 862
Db 694 -----CTGGACACAGTGGGATGTGATGCTCTGTC-----CCTGGCCCCCATGCGCGCA 744
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863 GGTATTATCTGGTTTCATGCGATTCACAGACAGCGGTGTGGGACACTCGTGTGCAAGCC 922  
 745 CGTTTGTGTGAGCGCCTGTGATGCTCTATCAAGCTGTGGACGCTGGGGATTCCATGT 804  
 923 GAGCAGTGGTACCTTTTCATGTCACGAGGAGATGTTAATACGGTCAAGTTCTTTCCGG 982  
 805 GCCGA---CAGACCTTTCATCGGCCATGAATCCGACATCAATGCAATGCGTTTCTTCCCA 861  
 983 ATGGGTATAGATTGGGACTGTGATCAGACGATGGAACATGACAGGCTGTATGACATAAGGA 1042  
 862 AGGGCTACGCTTACCACCGGCTCTGACGACGCCACGTCGCGCTCTTCGACCTGCGGG 921  
 1043 CTGGTCAACAACTCAGGCTGTATACGCCACATGTTGTTGAGTGTGAGAACGACCTGTCACT 1102  
 922 CGGATCAGGAGCTCTCATGTACTCCCA-----TGACAAACATCATCTGTGGCATCACT 975  
 1103 CCAATTGCATCTCTGTGTCAGGAGACTTCTTTTCGCTGGCTATCGGACCAACACTT 1162  
 976 CTGTTGCTCTCTGCGCAGCGACGCGCTGCTGCTGCTGGCTACGACGACTTCAAC---T 1032  
 1163 GCTACGTTGGGATACCTCTTTGGGAGAGGTTGTTATTTGGATTGGGATTACAGCAGGATT 1222  
 1033 GCAACATCTGGGATGCCATGAAGGCGACCGTCGAGGATCTCTCGC-----TG 1080  
 1223 CACACAGGAATAGAATAAGCTGTTTGGGTTGTACAGCAGATGGAAGTGCATTTGTGTACAG 1282  
 1081 GCCACGACAAACCGGTGAGCTGCTCGGGGTCAACGACGATGGCATGGCTGTGGCCACGG 1140  
 1283 GAAGTTGGGATTCMAATCTTAAGATATGG 1311  
 1141 GCTCTGGGACTCTTCTCTCAAGATCTGG 1169

RESULT 9  
 US-09-803-653-4  
 ; Sequence 4, Application US/09803653  
 ; Patent No. 6924100  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Siffert, Winfried  
 ; TITLE OF INVENTION: GENE ALTERATION IN THE GENE FOR THE GBETA3-SUBUNIT OF THE HUMAN G  
 ; FILE REFERENCE: 741135-12  
 ; CURRENT APPLICATION NUMBER: US/09/803,653  
 ; CURRENT FILING DATE: 2001-03-12  
 ; PRIOR APPLICATION NUMBER: PCT/EP99/06534  
 ; PRIOR FILING DATE: 1999-09-06  
 ; PRIOR APPLICATION NUMBER: DE 198 41 299.1  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: DE 199 04 825.8  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: DE 199 12 049.8  
 ; PRIOR FILING DATE: 1999-03-18  
 ; PRIOR APPLICATION NUMBER: DE 199 14 229.7  
 ; PRIOR FILING DATE: 1999-03-29  
 ; PRIOR APPLICATION NUMBER: DE 199 19 989.2  
 ; PRIOR FILING DATE: 1999-04-30  
 ; PRIOR APPLICATION NUMBER: DE 199 23 539.2  
 ; PRIOR FILING DATE: 1999-05-21  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 894  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-803-653-4

Query Match 5.9%; Score 96; DB 3; Length 894;  
 Best Local Similarity 55.7%; Pred. No. 1e-20;  
 Matches 233; Conservative 0; Mismatches 170; Indels 15; Gaps 2;  
 380 GTGCTACTCTTCAGGGACACACCGGAAGGTTTATTCATTAGATTGGACACCGGAGGGA 439  
 143 GCGGACGTTTAAGGGGACACCTGGCCAAAGATTTACGCCATGCACTGGGCACTGATTTCTA 202

440 ACCGATTGTGATGCTATCTCAAGATGGGAGATTAATCGTGTGGAATGCTCTTAAGAGTC 499  
 203 AGCTGCTGTAAGTGCCTCGCAAGATGGGAAGCTGATCGTGTGGACAGCTACACCA 262  
 500 AGAAAACTCATGCTATTAAACTCCCTGTGTCATGGGTTTATGACATGTCTTCTCTCCAA 559  
 263 ACAAGTGCAGCCATCCCATCTGCTCTCTGCTCATGACCTGTGCTATATGCCCAT 322  
 560 ATGCTAGTCCGTTCCGTTGCTGATTTAGACAGTGTATGTTCTATCTTTAGCCTTAGCT 619  
 323 CAGGGAACCTTTGTGTCATGTGGGGGCTGGACAAACATGTGTTCCATCTACAACTCAAT 382  
 620 CAACGGCGGACAGGATGAACTGTACCGGTTTCAAGAAATGCTCACTGCTCACAGGGAT 679  
 383 C-----CCGTGAGGGCAATGTCAAGGTCAAGCCGGAGCTTTCTGCTCACAGGTT 433  
 680 ATGTTTCTGCTGTCTCAGTATGTCCCAATGAGGATGCCACCTTATCAACAGTTTCAGGTG 739  
 434 ATCTCTCTGCTGCTGCTTCTCT-----GGATGACAAACATATTTGTGACAGCTCGGGG 487  
 740 ATCAAACTTGTATCTTATGGGATGTAATCTGCTCTCAAACTTCTGTTTTCGCGG 797  
 488 ACACCACGCTGTGCTTGTGGGACATTTGAGACTGGGCGACGAGAAGACTGTATTTGTGGG 545

RESULT 10  
 US-09-147-826B-1  
 ; Sequence 1, Application US/09147826B  
 ; Patent No. 6251853  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Siffert, Winfried  
 ; TITLE OF INVENTION: PTX-SENSITIVE G PROTEINS, THEIR PREPARATION AND USE  
 ; FILE REFERENCE: 1135-0003  
 ; CURRENT APPLICATION NUMBER: US/09/147,826B  
 ; CURRENT FILING DATE: 1999-03-15  
 ; PRIOR APPLICATION NUMBER: PCT/EP97/04709  
 ; PRIOR FILING DATE: 1997-08-29  
 ; PRIOR APPLICATION NUMBER: DE 196 37 518.5  
 ; PRIOR FILING DATE: 1996-09-13  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1394  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(897)  
 US-09-147-826B-1

Query Match 5.1%; Score 83.8; DB 3; Length 1394;  
 Best Local Similarity 58.0%; Pred. No. 1.5e-16;  
 Matches 148; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

380 GTGCTACTCTTCAGGGACACACCGGAAGGTTTATTCATTAGATTGGACACCGGAGGGA 439  
 143 GCGGACGTTTAAGGGGACACCTGGCCAAAGATTTACGCCATGCACTGGGCACTGATTTCTA 202  
 440 ACCGATTGTGATGCTATCTCAAGATGGGAGATTAATCGTGTGGAATGCTCTTAACGAGTC 499  
 203 AGCTGCTGTAAGTGCCTCGCAAGATGGGAAGTGTGTTGGGACAGCTACACCA 262  
 500 AGAAAACTCATGCTATTAAACTCCCTTTGTCATGGGTTATGACATGTGCTTTCTCTCAA 559  
 263 ACAAGTGCAGCCATCCCATCTGCTCTCTGCTCATGACCTGTGCTATGCCCAT 322  
 560 ATGCTCAGTCCGTTGCTGTTGAGATTAGACAGTGTATGTTCTATCTTTAGCCTTAGCT 619  
 323 CAGGGAACCTTTGTGTCATGTGGGGGCTGGACAAACATGTGTTCCATCTCAACCTCAAT 382  
 620 CAACGGCGGACAGG 634

Db 383 CCCGTGAGGCAATG 397

## RESULT 11

US-09-032-372-6  
; Sequence 6, Application US/09032372  
; Patent No. 6008337  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lai, Preeti  
; TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/032,372  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0478 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2119 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: SYNORAB01  
; CLONE: 78191  
US-09-032-372-6

Query Match 4.4%; Score 71.4; DB 3; Length 2119;  
Best Local Similarity 57.3%; Pred. No. 2.7e-12;  
Matches 129; Conservative 0; Mismatches 96; Indels 0; Gaps 0;  
QY 383 GTACTCTTCAGGACACACCGGAAAGGTTTATTCAATTAGATTGGACACCGGAGGACACC 442  
Db 362 GGACCTCAAGGCCACCGGAAACAAGTCCTGTGCATGACCTGGTGCAAGATAAGAGA 421  
QY 443 GGATTGTCAGTGCATCTCAAGATGGGAGATTAAATCGTGTGGAATGCTCTAACGAGTCAGA 502  
Db 422 GGATCGTGAGTCGTGCACAGATGGGAAGGTGATCGTGTGGGATTCCTTCACCACAACA 481  
QY 503 AAACATCATGCTATTAACTCCCTTGTGATGGGTTATGACATGCTTTCTCTCAAAATG 562  
Db 482 AGGAGCACCGGTCCACCATGCCCTGCACGTGGGTGATGCGCATGCTTTATGCCCATCGG 541  
QY 563 GTCAGTCGGTTCGCTGCTGGATTAGACAGTGTATGTTCTATCT 607  
Db 542 GATGTGCCATTGCTTGTGCTGGTTTGGATAATAAGTGTCTGTGT 586

## RESULT 12

US-09-016-434-1017  
; Sequence 1017, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1017:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 659 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: CERVNOT01  
; CLONE: 930839  
US-09-016-434-1017

Query Match 3.7%; Score 61; DB 3; Length 659;  
Best Local Similarity 53.0%; Pred. No. 3.3e-09;  
Matches 124; Conservative 0; Mismatches 110; Indels 0; Gaps 0;  
QY 383 GTACTCTTCAGGACACACCGGAAAGGTTTATTCAATTAGATTGGACACCGGAGGAAACC 442  
Db 312 GGACACTCGGGGGCACCTGGCCAAAGATCTNCGCCNTGCACTGGGGCACAGACTCCAGGC 371  
QY 443 GGATTGTCAGTGCATCTCAAGATGGGAGATTAAATCGTGTGGAATGCTCTAACGAGTCAGA 502  
Db 372 TTCTCGTCAGTGCCTCGCAGGATGGTAAACTTATCNTCTGGGACAGCTACGCCACCNACA 431  
QY 503 AAACCTCATGCTATTAAACTCCCTTGTGCATGGGTTATGACATGTGCTTTCTCTCCAAATG 562  
Db 432 AGGTCTCTCGCATCCCTCTGGCTCTCTCTGGGTCATGACCTGTGCAINTGCCCTTCTG 491  
QY 563 GTCAGTCGGTTCGCTGTGGTGGATTAGACAGTGTATGTTCTATCTTTAGCCTTA 616  
Db 492 GGAACATATGTGGCTGGGTGGCCTGGATAACATTTGCTCCATTACAAATCTGA 545

## RESULT 13

US-09-270-767-53/c

	Query Match	3.6%	Score 58.2;	DB 3;	Length 551;
	Best Local Similarity	52.2%;	Pred. No. 2.5e-08;		
	Matches 129;	Conservative 0;	Mismatches 118;	Indels 0;	Gaps 0;
Qy	388	CTTCAGGGACACACCGGAAGGTTTATTCATTAGATTGGACACCGGAGAGGACCGGATT	447		
Db	460	CTCAAGGGCCACACGAGGCTCTGTGCACCGACTGGAGTCCGACACAGCGTCACATC	401		
Qy	448	GTCAGTGCATCTCAAGATGGGAGATTAATCTGTGGATGCTCTAAACGATGCAGAAACT	507		
Db	400	ATCTCCTCGTCGACGACGACGCTCTGATCATCTGGGATGCTTCAACCACGAACAGGAG	341		
Qy	508	CATGCTATTAACCTCCCTTGTGCATGGGTTATGACATGTGCTTCTCTCCAAATGGTCAG	567		

Search completed: December 28, 2005, 19:32:47  
Job time : 324 secs

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